

Val	Ile	Ser	Asp	Pro	Ala	Asp	Pro	Arg	Leu	Asp	Asp	Val	Arg	Asp	Leu	
				10					15						20	
aac	cat	tcc	gat	tcc	cgg	cca	gac	cta	ccc	ggg	ggc	aaa	ggc	ctt	gtt	211
Asn	His	Ser	Asp	Ser	Arg	Pro	Asp	Leu	Pro	Gly	Gly	Lys	Gly	Leu	Val	
			25					30					35			
gtt	gcc	gaa	ggg	ccg	ttg	gtg	gtt	ggg	cgg	ctt	ctg	gaa	tcg	cgt	tac	259
Val	Ala	Glu	Gly	Pro	Leu	Val	Val	Gly	Arg	Leu	Leu	Glu	Ser	Arg	Tyr	
		40					45					50				
cca	gtg	cgt	gcg	atc	gtc	ggg	ttt	aaa	aac	aag	ctg	gat	tct	ttc	ctc	307
Pro	Val	Arg	Ala	Ile	Val	Gly	Phe	Lys	Asn	Lys	Leu	Asp	Ser	Phe	Leu	
	55					60					65					
gac	agc	atc	gat	gca	tcc	ctt	gtt	gaa	ggc	atc	cca	gtg	tat	gag	gta	355
Asp	Ser	Ile	Asp	Ala	Ser	Leu	Val	Glu	Gly	Ile	Pro	Val	Tyr	Glu	Val	
70					75				80						85	
tcc	cgc	gag	ctc	ctc	gca	gag	gtc	gca	ggg	ttt	gat	atg	cac	cgc	gga	403
Ser	Arg	Glu	Leu	Leu	Ala	Glu	Val	Ala	Gly	Phe	Asp	Met	His	Arg	Gly	
			90						95					100		
ctt	ctg	gcg	aca	gcc	gat	cgc	acc	gag	gaa	gca	agt	gtt	gcg	cag	gtt	451
Leu	Leu	Ala	Thr	Ala	Asp	Arg	Thr	Glu	Glu	Ala	Ser	Val	Ala	Gln	Val	
			105					110					115			
cta	gaa	aac	gcc	cgc	acc	gtg	gtg	gtg	ctg	gaa	ggc	gta	ggc	gat	cac	499
Leu	Glu	Asn	Ala	Arg	Thr	Val	Val	Val	Leu	Glu	Gly	Val	Gly	Asp	His	
		120					125					130				
gaa	aac	atc	gga	tcc	atg	ttc	cgc	aac	gca	gca	ggc	atg	ggc	gtt	gac	547
Glu	Asn	Ile	Gly	Ser	Met	Phe	Arg	Asn	Ala	Ala	Gly	Met	Gly	Val	Asp	
	135					140					145					
gcc	atc	ttg	ttc	ggc	aac	ggg	tgt	gcc	gat	cct	ttg	tat	cga	cgt	gtc	595
Ala	Ile	Leu	Phe	Gly	Asn	Gly	Cys	Ala	Asp	Pro	Leu	Tyr	Arg	Arg	Val	
150					155					160					165	
gtt	cga	gtc	tca	atg	ggc	cac	gtg	ctc	cgc	ctg	ccg	ttc	gca	cac	ttg	643
Val	Arg	Val	Ser	Met	Gly	His	Val	Leu	Arg	Leu	Pro	Phe	Ala	His	Leu	
				170					175					180		
gaa	ggc	acc	tac	acc	acg	tgg	cag	cgc	agc	tta	gag	cag	ctc	aaa	gaa	691
Glu	Gly	Thr	Tyr	Thr	Thr	Trp	Gln	Arg	Ser	Leu	Glu	Gln	Leu	Lys	Glu	
			185					190					195			
gcc	gga	ttc	cac	ctc	gtt	tca	ctc	acc	cca	gat	cca	gag	gcg	gaa	cac	739
Ala	Gly	Phe	His	Leu	Val	Ser	Leu	Thr	Pro	Asp	Pro	Glu	Ala	Glu	His	
		200					205					210				
ctc	gaa	gat	gcg	ctc	gca	ggc	aaa	gac	aaa	gtg	gct	cta	ctc	gtg	ggc	787
Leu	Glu	Asp	Ala	Leu	Ala	Gly	Lys	Asp	Lys	Val	Ala	Leu	Leu	Val	Gly	
	215					220					225					
gct	gaa	ggc	cca	ggc	ctg	acc	gag	cat	gcg	atg	cgc	gcc	acc	gat	gtc	835
Ala	Glu	Gly	Pro	Gly	Leu	Thr	Glu	His	Ala	Met	Arg	Ala	Thr	Asp	Val	
230					235					240					245	
cgc	gcc	cgc	atc	ccg	atg	gcg	ccg	ggg	acc	gat	agc	ttg	aac	ctg	gct	883
Arg	Ala	Arg	Ile	Pro	Met	Ala	Pro	Gly	Thr	Asp	Ser	Leu	Asn	Leu	Ala	

250 255 260

acc tcg gcg gcg att gcg ttt tat gaa cgg gat cgc tca cag cgt 928  
Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp Arg Ser Gln Arg  
265 270 275

taagtaacag cgctaagtag tag 951

<210> 278  
<211> 276  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 278

Met Thr Thr Arg Thr Val Ile Ser Asp Pro Ala Asp Pro Arg Leu Asp  
1 5 10 15

Asp Val Arg Asp Leu Asn His Ser Asp Ser Arg Pro Asp Leu Pro Gly  
20 25 30

Gly Lys Gly Leu Val Val Ala Glu Gly Pro Leu Val Val Gly Arg Leu  
35 40 45

Leu Glu Ser Arg Tyr Pro Val Arg Ala Ile Val Gly Phe Lys Asn Lys  
50 55 60

Leu Asp Ser Phe Leu Asp Ser Ile Asp Ala Ser Leu Val Glu Gly Ile  
65 70 75 80

Pro Val Tyr Glu Val Ser Arg Glu Leu Leu Ala Glu Val Ala Gly Phe  
85 90 95

Asp Met His Arg Gly Leu Leu Ala Thr Ala Asp Arg Thr Glu Glu Ala  
100 105 110

Ser Val Ala Gln Val Leu Glu Asn Ala Arg Thr Val Val Val Leu Glu  
115 120 125

Gly Val Gly Asp His Glu Asn Ile Gly Ser Met Phe Arg Asn Ala Ala  
130 135 140

Gly Met Gly Val Asp Ala Ile Leu Phe Gly Asn Gly Cys Ala Asp Pro  
145 150 155 160

Leu Tyr Arg Arg Val Val Arg Val Ser Met Gly His Val Leu Arg Leu  
165 170 175

Pro Phe Ala His Leu Glu Gly Thr Tyr Thr Thr Trp Gln Arg Ser Leu  
180 185 190

Glu Gln Leu Lys Glu Ala Gly Phe His Leu Val Ser Leu Thr Pro Asp  
195 200 205

Pro Glu Ala Glu His Leu Glu Asp Ala Leu Ala Gly Lys Asp Lys Val  
210 215 220

Ala Leu Leu Val Gly Ala Glu Gly Pro Gly Leu Thr Glu His Ala Met  
225 230 235 240

Arg Ala Thr Asp Val Arg Ala Arg Ile Pro Met Ala Pro Gly Thr Asp

245

250

255

Ser Leu Asn Leu Ala Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp  
 260 265 270

Arg Ser Gln Arg  
 275

&lt;210&gt; 279

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(643)

&lt;223&gt; RXA02522

&lt;400&gt; 279

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aacgattcca ccggtattaa acattgctga aatagggcgg atg tgg gct cgt gac 115  
 Met Trp Ala Arg Asp  
 1 5

ata aac ttt cta tac atg agt aca gag cag gaa ctg caa atc gga aaa 163  
 Ile Asn Phe Leu Tyr Met Ser Thr Glu Gln Glu Leu Gln Ile Gly Lys  
 10 15 20

gtt gta aaa tcc cac ggc att cgg ggt gaa gtc gtg gtg gaa ttg agc 211  
 Val Val Lys Ser His Gly Ile Arg Gly Glu Val Val Val Glu Leu Ser  
 25 30 35

acc gat gat cca gac att cgc ttc gcc att ggg gaa gtt ctc aac ggc 259  
 Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly Glu Val Leu Asn Gly  
 40 45 50

aag cag gca ggc aag gag cat tca ctg acc atc gat gca gcg cgc atg 307  
 Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile Asp Ala Ala Arg Met  
 55 60 65

cac caa ggt cga ctc ttg gtg aag ttc gca gag gtc cca gat cgt acc 355  
 His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu Val Pro Asp Arg Thr  
 70 75 80 85

gct gct gat tct ttg cgt gga act cga ttc ttt gcg gca cct ctt gag 403  
 Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe Ala Ala Pro Leu Glu  
 90 95 100

gat gaa gac gat gag gat ggc ttc tac gac cat gag ttg gaa ggt ctg 451  
 Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His Glu Leu Glu Gly Leu  
 105 110 115

cgc gtc att cac gag ggc gag gat atc ggt gaa gtc acc ggc gtg atg 499  
 Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu Val Thr Gly Val Met  
 120 125 130

cat ggc cca gcc ggt gag atc ctg gaa gtc cgc ctg acc tca ggc aag 547  
 His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg Leu Thr Ser Gly Lys  
 135 140 145

gaa aca ctg att cct ttt gtg cac gcc att gtt cct gag gtg gat ctg 595  
Glu Thr Leu Ile Pro Phe Val His Ala Ile Val Pro Glu Val Asp Leu  
150 155 160 165

gaa gaa gga acc gca acg atc acc cct cca gag ggc ttg tta gat ctt 643  
Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu Gly Leu Leu Asp Leu  
170 175 180

taggctccga cagatttaat agt 666

<210> 280

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Met Trp Ala Arg Asp Ile Asn Phe Leu Tyr Met Ser Thr Glu Gln Glu  
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Leu Gln Ile Gly Lys Val Val Lys Ser His Gly Ile Arg Gly Glu Val  
20 25 30

Val Val Glu Leu Ser Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly  
35 40 45

Glu Val Leu Asn Gly Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile  
50 55 60

Asp Ala Ala Arg Met His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu  
65 70 75 80

Val Pro Asp Arg Thr Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe  
85 90 95

Ala Ala Pro Leu Glu Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His  
100 105 110

Glu Leu Glu Gly Leu Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu  
115 120 125

Val Thr Gly Val Met His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg  
130 135 140

Leu Thr Ser Gly Lys Glu Thr Leu Ile Pro Phe Val His Ala Ile Val  
145 150 155 160

Pro Glu Val Asp Leu Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu  
165 170 175

Gly Leu Leu Asp Leu  
180

<210> 281

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>



<221> CDS  
 <222> (101)..(1060)  
 <223> RXA00717

<400> 281

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tcaatttcat acgtttttctc tcaagattaa ggacacttac gtg acc cca ccc gct 115
                               Val Thr Pro Pro Ala
                               1                               5

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga 163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly
                               10                               15                               20

tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac 211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn
                               25                               30                               35

aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct 259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala
                               40                               45                               50

aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg 307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met
                               55                               60                               65

ggg ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg 355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val
                               70                               75                               80                               85

ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att 403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile
                               90                               95                               100

gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc 451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly
                               105                               110                               115

gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc 499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg
                               120                               125                               130

atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt 547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg
                               135                               140                               145

ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt 595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly
                               150                               155                               160                               165

gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc 643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val
                               170                               175                               180

ggg cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat 691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp
                               185                               190                               195

ggg gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag 739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys

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200	205	210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc			787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser			
215	220	225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac			835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp			
230	235	240	245
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc			883
Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile			
250	255	260	
gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag			931
Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu			
265	270	275	
ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt			979
Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val			
280	285	290	
cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct			1027
Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser			
295	300	305	
gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg			1080
Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu			
310	315	320	
cct			1083
<210> 282			
<211> 320			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 282			
Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser			
1	5	10	15
Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly			
20	25	30	
Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile			
35	40	45	
Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp			
50	55	60	
Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val			
65	70	75	80
Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His			
85	90	95	
Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile			
100	105	110	
Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg			

115					120					125					
Val	Asp	Gly	Val	Arg	Ile	His	Ile	Asn	Glu	Asp	Leu	Glu	Tyr	Phe	Val
130						135					140				
Leu	Asn	Lys	Pro	Arg	Gly	Met	His	Ser	Thr	Met	Ser	Asp	Glu	Leu	Gly
145					150					155					160
Arg	Pro	Cys	Val	Gly	Asp	Leu	Val	Ser	Glu	Lys	Thr	Ala	Ser	Gly	Gln
				165					170					175	
Arg	Leu	Phe	His	Val	Gly	Arg	Leu	Asp	Ala	Asp	Thr	Glu	Gly	Leu	Leu
			180					185					190		
Leu	Leu	Thr	Asn	Asp	Gly	Glu	Leu	Ala	Asn	Arg	Leu	Met	His	Pro	Lys
		195					200					205			
Tyr	Glu	Val	Ser	Lys	Thr	Tyr	Leu	Ala	Thr	Val	Arg	Gly	Glu	Ala	Thr
	210					215					220				
Asn	Lys	Leu	Val	Ser	Ala	Leu	Arg	Asp	Gly	Val	Glu	Leu	Glu	Asp	Gly
225					230					235					240
Pro	Ala	Lys	Ala	Asp	Phe	Ala	Gln	Ile	Ile	Asp	Val	Phe	Gln	Gly	Lys
				245					250					255	
Ser	Leu	Leu	Arg	Ile	Glu	Ile	His	Glu	Gly	Arg	Lys	His	Ile	Val	Arg
			260					265					270		
Arg	Leu	Phe	Asp	Glu	Leu	Gly	Phe	Pro	Val	Glu	Arg	Leu	Val	Arg	Thr
		275					280					285			
Lys	Leu	His	Thr	Val	Gln	Leu	Gly	Asp	Gln	Lys	Pro	Gly	Ser	Leu	Arg
	290					295					300				
Ala	Leu	Asn	Ser	Ser	Glu	Leu	Thr	Ser	Leu	Tyr	Lys	Val	Val	Gln	Leu
305					310					315					320

&lt;210&gt; 283

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(736)

&lt;223&gt; RXA02615

&lt;400&gt; 283

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gaaataggac	aaaacgcgat	tctatgacta	tattcatctc	atg	caa	ttc	gca	caa	115
				Met	Gln	Phe	Ala	Gln	
				1				5	

aac	ccg	cgt	ctg	acg	aac	gac	gcg	gtg	atc	tta	gaa	cca	ctg	tca	cat	163
Asn	Pro	Arg	Leu	Thr	Asn	Asp	Ala	Val	Ile	Leu	Glu	Pro	Leu	Ser	His	

10										15					20					
cag	tgg	act	cag	gat	ctc	cag	gaa	gct	gtc	gcc	tca	caa	gaa	ttg	tgg	211				
Gln	Trp	Thr	Gln	Asp	Leu	Gln	Glu	Ala	Val	Ala	Ser	Gln	Glu	Leu	Trp					
			25						30			35								
cgc	cat	tgg	ttc	gtc	gct	cta	ccc	acc	cca	gag	ggc	atg	gcg	gag	gaa	259				
Arg	His	Trp	Phe	Val	Ala	Leu	Pro	Thr	Pro	Glu	Gly	Met	Ala	Glu	Glu					
			40						45			50								
att	gac	cgc	cgc	cta	gcc	gaa	cat	gca	gac	gga	ctg	tgt	gcg	cct	tgg	307				
Ile	Asp	Arg	Arg	Leu	Ala	Glu	His	Ala	Asp	Gly	Leu	Cys	Ala	Pro	Trp					
			55						60			65								
gca	atc	att	tcc	gct	gca	aca	ggc	cgt	gcc	gtt	ggc	atg	acc	tca	ttt	355				
Ala	Ile	Ile	Ser	Ala	Ala	Thr	Gly	Arg	Ala	Val	Gly	Met	Thr	Ser	Phe					
			70						75			80			85					
cat	acc	ctt	gac	cac	gcg	aat	aaa	cgg	ctg	gaa	att	gga	cgc	aca	tgg	403				
His	Thr	Leu	Asp	His	Ala	Asn	Lys	Arg	Leu	Glu	Ile	Gly	Arg	Thr	Trp					
			90						95			100								
atg	gct	gcc	cat	gtc	caa	gga	acc	ggc	atc	aac	ccc	tcg	gtg	aaa	ttc	451				
Met	Ala	Ala	His	Val	Gln	Gly	Thr	Gly	Ile	Asn	Pro	Ser	Val	Lys	Phe					
			105						110			115								
ctg	cag	ttg	cag	cgc	gct	ttt	gaa	gac	ctc	ggg	gtc	aat	gcc	gtg	gaa	499				
Leu	Gln	Leu	Gln	Arg	Ala	Phe	Glu	Asp	Leu	Gly	Val	Asn	Ala	Val	Glu					
			120						125			130								
ttc	cga	acg	aac	tgg	cac	aac	cac	cgc	tcc	cgc	gcc	gca	atc	gaa	cga	547				
Phe	Arg	Thr	Asn	Trp	His	Asn	His	Arg	Ser	Arg	Ala	Ala	Ile	Glu	Arg					
			135						140			145								
ctc	gga	gca	aaa	caa	gac	ggc	gta	cta	cgc	aaa	cat	cgc	atc	cac	cct	595				
Leu	Gly	Ala	Lys	Gln	Asp	Gly	Val	Leu	Arg	Lys	His	Arg	Ile	His	Pro					
			150						155			160			165					
gac	ggc	acc	gtc	cgc	gac	acc	gtc	atc	tat	tcc	atc	acc	aac	gat	gaa	643				
Asp	Gly	Thr	Val	Arg	Asp	Thr	Val	Ile	Tyr	Ser	Ile	Thr	Asn	Asp	Glu					
			170						175			180								
tgg	cct	gcc	gtc	aaa	ctg	acg	ctc	atg	gag	cga	ctg	tac	cgt	cac	atg	691				
Trp	Pro	Ala	Val	Lys	Leu	Thr	Leu	Met	Glu	Arg	Leu	Tyr	Arg	His	Met					
			185						190			195								
cag	gtt	ccc	atc	att	ccc	aac	gag	gca	tcg	ctt	ttc	gac	gcc	agc		736				
Gln	Val	Pro	Ile	Ile	Pro	Asn	Glu	Ala	Ser	Leu	Phe	Asp	Ala	Ser						
			200						205			210								
tagcccccttt gttcacccaa acc															759					

&lt;210&gt; 284

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 284

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1				5					10					15	

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Lys Ala Tyr Arg Glu Ala Ala Glu Lys Ile Asp Ala Gly Arg Ile Tyr  
10 15 20

tcc cca ctc gag gct gca aac ctg gtc aag gag acc tcc tcc aag aac 211  
 Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser Lys Asn  
 25 30 35

tac gac gct tcc atc gac gta gct atc cgc ctg ggc gtt gac cca cgt 259  
 Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp Pro Arg  
 40 45 50

aag gct gat cag ctt gtt cgt ggc acc gtc tcc ctg cct aac ggc acc 307  
 Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn Gly Thr  
 55 60 65

ggt aag acc gtt cgc gtt gct gtg ttc gca cag ggc gag aag gct act 355  
 Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys Ala Thr  
 70 75 80 85

gag gct gag gct gct ggc gct gac ttc gtt ggc acc gac gag ctc gtt 403  
 Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu Leu Val  
 90 95 100

gag aag atc cag ggt ggc tgg acc gac ttc gac gtt gct att gca acc 451  
 Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile Ala Thr  
 105 110 115

cct gat cag atg gct aag atc ggc cgt atc gct cgt gtc ttg ggc cca 499  
 Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu Gly Pro  
 120 125 130

cgt ggt ctg atg cct aac cct aag acc ggc acc gtc acc aac gat gtc 547  
 Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn Asp Val  
 135 140 145

gct aag gct atc gaa gag gtc aag ggc ggc aag att tcc ttc cgc gtt 595  
 Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe Arg Val  
 150 155 160 165

gac aag gct tcc aac ctg cac gct gca att ggt aag gct tcc ttc gat 643  
 Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser Phe Asp  
 170 175 180

gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag atc atc 691  
 Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu Ile Ile  
 185 190 195

cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc gtg acc 739  
 Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg Val Thr  
 200 205 210

ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac gtc acc 787  
 Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His Val Thr  
 215 220 225

aag aac tac gca gaa gag gca taagccttcc cacgcgtaac tct 831  
 Lys Asn Tyr Ala Glu Glu Ala  
 230 235

&lt;210&gt; 286

&lt;211&gt; 236

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 286

Met Ser Lys Asn Ser Lys Ala Tyr Arg Glu Ala Ala Glu Lys Ile Asp  
1 5 10 15  
Ala Gly Arg Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu  
20 25 30  
Thr Ser Ser Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu  
35 40 45  
Gly Val Asp Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser  
50 55 60  
Leu Pro Asn Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln  
65 70 75 80  
Gly Glu Lys Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly  
85 90 95  
Thr Asp Glu Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp  
100 105 110  
Val Ala Ile Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala  
115 120 125  
Arg Val Leu Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr  
130 135 140  
Val Thr Asn Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys  
145 150 155 160  
Ile Ser Phe Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly  
165 170 175  
Lys Ala Ser Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu  
180 185 190  
Leu Asp Glu Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr  
195 200 205  
Val Lys Arg Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val  
210 215 220  
Asp Thr His Val Thr Lys Asn Tyr Ala Glu Glu Ala  
225 230 235

<210> 287

<211> 674

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(651)

<223> FRXA01343

<400> 287

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Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser
 1          5          10          15
aag aac tac gac gct tcc atc gac gta gct atc cgc ctg ggc gtt gac 96
Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp
          20          25          30
cca cgt aag gct gat cag ctt gtt cgt ggc acc gtc tcc ctg cct aac 144
Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn
          35          40          45
ggc acc ggt aag acc gtt cgc gtt gct gtg ttc gca cag ggc gag aag 192
Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys
          50          55          60
gct act gag gct gag gct gct ggc gct gac ttc gtt ggc acc gac gag 240
Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu
          65          70          75          80
ctc gtt gag aag atc cag ggt ggc tgg acc gac ttc gac gtt gct att 288
Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile
          85          90          95
gca acc cct gat cag atg gct aag atc ggc cgt atc gct cgt gtc ttg 336
Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu
          100          105          110
ggc cca cgt ggt ctg atg cct aac cct aag acc ggc acc gtc acc aac 384
Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn
          115          120          125
gat gtc gct aag gct atc gaa gag gtc aag ggc ggc aag att tcc ttc 432
Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe
          130          135          140
cgc gtt gac aag gct tcc aac ctg cac gct gca att ggt aag gct tcc 480
Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser
          145          150          155          160
ttc gat gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag 528
Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu
          165          170          175
atc atc cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc 576
Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg
          180          185          190
gtg acc ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac 624
Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His
          195          200          205
gtc acc aag aac tac gca gaa gag gca taagccttcc cacgcgtaac 671
Val Thr Lys Asn Tyr Ala Glu Ala
          210          215
tct 674

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&lt;210&gt; 288

&lt;211&gt; 217

&lt;212&gt; PRT



<213> Corynebacterium glutamicum

<400> 288

Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser  
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Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp  
20 25 30

Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn  
35 40 45

Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys  
50 55 60

Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu  
65 70 75 80

Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile  
85 90 95

Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu  
100 105 110

Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn  
115 120 125

Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe  
130 135 140

Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser  
145 150 155 160

Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu  
165 170 175

Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg  
180 185 190

Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His  
195 200 205

Val Thr Lys Asn Tyr Ala Glu Glu Ala  
210 215

<210> 289

<211> 684

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(661)

<223> RXA01951

<400> 289

cgctaccgcg tcacgcactt ccgtcgtaac gacaaggatg gcgtattggc aaaggctcgct 60

cacatcgagt acgacccaaa ccgtaccgct aacattgcac ttg ctt cac tac ttc 115  
Leu Leu His Tyr Phe

	1	5	
gat ggc gag aag cgt tac atc ctc gca ccg aag ggc ctg acc cag ggc			163
Asp Gly Glu Lys Arg Tyr Ile Leu Ala Pro Lys Gly Leu Thr Gln Gly			
	10	20	
acc gtt atc gag tcc ggc gct gca gcc gac atc aag gtt ggt aac aac			211
Thr Val Ile Glu Ser Gly Ala Ala Ala Asp Ile Lys Val Gly Asn Asn			
	25	30	35
ctg cca ctg cgt aac atc ccg act ggt acc acc atc cac aac gtg gag			259
Leu Pro Leu Arg Asn Ile Pro Thr Gly Thr Thr Ile His Asn Val Glu			
	40	45	50
ttg aag cca ggc gca ggt gca aag ctg gca cgt tcc gct gga gct tcc			307
Leu Lys Pro Gly Ala Gly Ala Lys Leu Ala Arg Ser Ala Gly Ala Ser			
	55	60	65
atc cag ctt ctt ggt aag gaa ggc tcc tac gca gtt ctg cgt atg cca			355
Ile Gln Leu Leu Gly Lys Glu Gly Ser Tyr Ala Val Leu Arg Met Pro			
	70	75	80
tcc tcc gag atc cga cgc gta aac atc cgc tgc cgc gcg act gtt ggt			403
Ser Ser Glu Ile Arg Arg Val Asn Ile Arg Cys Arg Ala Thr Val Gly			
	90	95	100
gag gtc ggc aac gcc gag cag atc aac att cgt tgg ggt aaa gct ggt			451
Glu Val Gly Asn Ala Glu Gln Ile Asn Ile Arg Trp Gly Lys Ala Gly			
	105	110	115
cgt atg cgt tgg aag ggc tgg cgc cca acc gtc cgt ggt gtc gtt atg			499
Arg Met Arg Trp Lys Gly Trp Arg Pro Thr Val Arg Gly Val Val Met			
	120	125	130
aac ccg gtc gac cac cca cac ggt ggt ggt gaa ggt aag act tct ggt			547
Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Lys Thr Ser Gly			
	135	140	145
ggt cgc cac cca gtc tcc cca tgg gga cag aag gaa ggc cgc acc cgc			595
Gly Arg His Pro Val Ser Pro Trp Gly Gln Lys Glu Gly Arg Thr Arg			
	150	155	160
aag cct aag cgt tac agc gat gac atg atc gtt cgt cgc cgt cgt gct			643
Lys Pro Lys Arg Tyr Ser Asp Asp Met Ile Val Arg Arg Arg Ala			
	170	175	180
aac aag aac aag aag cgt taagaggagg taacggtgaa tgt			684
Asn Lys Asn Lys Lys Arg			
	185		

&lt;210&gt; 290

&lt;211&gt; 187

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 290

Leu	Leu	His	Tyr	Phe	Asp	Gly	Glu	Lys	Arg	Tyr	Ile	Leu	Ala	Pro	Lys
1															15

Gly	Leu	Thr	Gln	Gly	Thr	Val	Ile	Glu	Ser	Gly	Ala	Ala	Ala	Asp	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30					
Lys	Val	Gly	Asn	Asn	Leu	Pro	Leu	Arg	Asn	Ile	Pro	Thr	Gly	Thr	Thr
		35					40					45			
Ile	His	Asn	Val	Glu	Leu	Lys	Pro	Gly	Ala	Gly	Ala	Lys	Leu	Ala	Arg
	50					55					60				
Ser	Ala	Gly	Ala	Ser	Ile	Gln	Leu	Leu	Gly	Lys	Glu	Gly	Ser	Tyr	Ala
	65				70					75					80
Val	Leu	Arg	Met	Pro	Ser	Ser	Glu	Ile	Arg	Arg	Val	Asn	Ile	Arg	Cys
				85					90					95	
Arg	Ala	Thr	Val	Gly	Glu	Val	Gly	Asn	Ala	Glu	Gln	Ile	Asn	Ile	Arg
			100					105					110		
Trp	Gly	Lys	Ala	Gly	Arg	Met	Arg	Trp	Lys	Gly	Trp	Arg	Pro	Thr	Val
		115					120					125			
Arg	Gly	Val	Val	Met	Asn	Pro	Val	Asp	His	Pro	His	Gly	Gly	Gly	Glu
	130					135					140				
Gly	Lys	Thr	Ser	Gly	Gly	Arg	His	Pro	Val	Ser	Pro	Trp	Gly	Gln	Lys
	145				150					155					160
Glu	Gly	Arg	Thr	Arg	Lys	Pro	Lys	Arg	Tyr	Ser	Asp	Asp	Met	Ile	Val
				165					170					175	
Arg	Arg	Arg	Arg	Ala	Asn	Lys	Asn	Lys	Lys	Arg					
			180					185							

<210> 291  
 <211> 507  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(484)  
 <223> FRXA01950

<400> 291  
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 cggtccgctc gcttaagacg tcgatagaaa aggacacatt atg gct att cgt aag 115  
 Met Ala Ile Arg Lys 5  
 tac aag ccg aca acc ccg ggt cgc cgc gca agc tcc gtt tcc atg ttc 163  
 Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser Ser Val Ser Met Phe 20  
 acg gag atc acc cgt tcg acc cct gag aag tca ctt ctc cgc cca ctg 211  
 Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser Leu Leu Arg Pro Leu 35  
 agc aag acc ggc gga cgt aac tct cac ggc cac atc acc acc cgt cac 259  
 Ser Lys Thr Gly Gly Arg Asn Ser His Gly His Ile Thr Thr Arg His 50

cgc ggt ggt gga cac aag cgc cgc tac cgc gtc atc gac ttc cgt cgt 307  
 Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val Ile Asp Phe Arg Arg  
 55 60 65  
 aac gac aag gat ggc gta ttg gca aag gtc gct cac atc gag tac gac 355  
 Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala His Ile Glu Tyr Asp  
 70 75 80 85  
 cca aac cgt acc gct aac att gca ctt gct tca cta ctt cga tgg cga 403  
 Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser Leu Leu Arg Trp Arg  
 90 95 100  
 gaa gcg tta cat cct cgc acc gaa ggg cct gac cca ggg cac cgt tat 451  
 Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp Pro Gly His Arg Tyr  
 105 110 115  
 cga gtc cgg cgc tgc agc cga cat caa ggt tgg taacaacctg ccactgcgta 504  
 Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp  
 120 125

aca

507

&lt;210&gt; 292

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 292

Met Ala Ile Arg Lys Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser  
1 5 10 15

Ser Val Ser Met Phe Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser  
20 25 30

Leu Leu Arg Pro Leu Ser Lys Thr Gly Gly Arg Asn Ser His Gly His  
35 40 45

Ile Thr Thr Arg His Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val  
50 55 60

Ile Asp Phe Arg Arg Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala  
65 70 75 80

His Ile Glu Tyr Asp Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser  
85 90 95

Leu Leu Arg Trp Arg Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp  
100 105 110

Pro Gly His Arg Tyr Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp  
115 120 125

&lt;210&gt; 293

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(754)

&lt;223&gt; RXA01286

&lt;400&gt; 293

cgccgaagac tgttgatgcc cttatgcgca tcgaccttcc ggccagcgtc gacgtgaaca 60

ttcagtgatc gacggaatct ttggcagcgg agaataaata atg agt gaa aac gag 115  
Met Ser Glu Asn Glu  
1 5

atc aag ggc att ctg ggc acc aag ctc ggc atg act cag atc ttc gac 163  
Ile Lys Gly Ile Leu Gly Thr Lys Leu Gly Met Thr Gln Ile Phe Asp  
10 15 20

gag gag aac cgc gtt att ccg gtt acc gtc gtt gaa gcg ggt cca tgc 211  
Glu Glu Asn Arg Val Ile Pro Val Thr Val Val Glu Ala Gly Pro Cys  
25 30 35

gta gtt tcc cag att cgc acc gtt gag acc gat ggc tac aac gcc atc 259  
Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp Gly Tyr Asn Ala Ile  
40 45 50

cag atc gcc tac ggc gaa atc gac cca cgc aag gtg aac cag cca ttg 307  
Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys Val Asn Gln Pro Leu  
55 60 65

act ggt cac ttc aag aaa gca ggc gtt acc ccc cgc cgc cac gtc acc 355  
Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro Arg Arg His Val Thr  
70 75 80 85

gag att cgt atg gac gat gtc tcc ggt tac gag gtt gga cag gac gtt 403  
Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu Val Gly Gln Asp Val  
90 95 100

acc gtt gaa atc ttc aac gac atc aag ttc gtt gac gtc acc ggt acc 451  
Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val Asp Val Thr Gly Thr  
105 110 115

acc aag ggt aag ggc tac gcc ggc gct atg aag cgc cat ggc ttc gct 499  
Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys Arg His Gly Phe Ala  
120 125 130

ggc cag ggt gcc ggc cac ggt aac cag gct gca cac cgc cgc gta ggt 547  
Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala His Arg Arg Val Gly  
135 140 145

ggc att ggt gca gct gct acc cca ggt cgc atc ttc aag ggc aag cgt 595  
Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile Phe Lys Gly Lys Arg  
150 155 160 165

atg gct ggc cgc atg ggt aat gac cgc gtc acc acc cag aac ctc aag 643  
Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr Thr Gln Asn Leu Lys  
170 175 180

gtt cag aag att gac gcc gat gcc aac atc atc ctt atc aag ggc gca 691  
Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile Leu Ile Lys Gly Ala  
185 190 195

atc cct ggt aac cgt ggt ggc atc gtt acc gtt aag acc gca gtg aag 739  
Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val Lys Thr Ala Val Lys  
200 205 210

ggc ggt gca cac gca tgacgaatct gaagctgtat gtt 777  
Gly Gly Ala His Ala  
215

<210> 294

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met Ser Glu Asn Glu Ile Lys Gly Ile Leu Gly Thr Lys Leu Gly Met  
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Thr Gln Ile Phe Asp Glu Glu Asn Arg Val Ile Pro Val Thr Val Val  
20 25 30

Glu Ala Gly Pro Cys Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp  
35 40 45

Gly Tyr Asn Ala Ile Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys  
50 55 60

Val Asn Gln Pro Leu Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro  
65 70 75 80

Arg Arg His Val Thr Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu  
85 90 95

Val Gly Gln Asp Val Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val  
100 105 110

Asp Val Thr Gly Thr Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys  
115 120 125

Arg His Gly Phe Ala Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala  
130 135 140

His Arg Arg Val Gly Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile  
145 150 155 160

Phe Lys Gly Lys Arg Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr  
165 170 175

Thr Gln Asn Leu Lys Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile  
180 185 190

Leu Ile Lys Gly Ala Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val  
195 200 205

Lys Thr Ala Val Lys Gly Gly Ala His Ala  
210 215

<210> 295

<211> 626

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(603)

&lt;223&gt; RXA01948

&lt;400&gt; 295

tct gta gaa ctc cct gca gag att ttt gac cgt gag gtc tcc gtc gca	48
Ser Val Glu Leu Pro Ala Glu Ile Phe Asp Arg Glu Val Ser Val Ala	
1 5 10 15	
ctg ctg cac cag gtt gtc aac gca cag ctt gca gca gct cga cag ggc	96
Leu Leu His Gln Val Val Asn Ala Gln Leu Ala Ala Ala Arg Gln Gly	
20 25 30	
acc cac tcc acc aag acc cgt ggc gaa gta cgt ggc ggt ggc cgt aag	144
Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Gly Arg Lys	
35 40 45	
cca ttc cgt cag aag gga acc ggt cgc gct cgt cag ggc tcg atc cgc	192
Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg	
50 55 60	
gca cct cac ttc acc ggt ggt ggc atc tcc cac ggc cct aag cca cgc	240
Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg	
65 70 75 80	
gac tac tct cag cgc acc cct aag aag atg atc aag gct gca ctt tac	288
Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr	
85 90 95	
ggt gca ctg tct gat cgt gca cgc aat gca cgt atc cac gtc gtc tcc	336
Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser	
100 105 110	
gaa ttg gtg cct ggc cag acc cct tcg acc aag tct gca aag gct ttc	384
Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe	
115 120 125	
atc gag cgt ctg acc gag cgt aag tcc gtg ctg ctc gta gtg agc cgt	432
Ile Glu Arg Leu Thr Glu Arg Lys Ser Val Leu Leu Val Val Ser Arg	
130 135 140	
gag gat atc aac gcc cag aag agt gct aac aac ctg cct ggc gtc cac	480
Glu Asp Ile Asn Ala Gln Lys Ser Ala Asn Asn Leu Pro Gly Val His	
145 150 155 160	
atc ctg gcc gct gat cag ctg aac acc tac gac gtt ctc aag tct gac	528
Ile Leu Ala Ala Asp Gln Leu Asn Thr Tyr Asp Val Leu Lys Ser Asp	
165 170 175	
gac gtt gtg ttc tcc gtt gag gct ctc cac acc ttc atc aac cgc gct	576
Asp Val Val Phe Ser Val Glu Ala Leu His Thr Phe Ile Asn Arg Ala	
180 185 190	
tcc ggt gcg gca cag gag gag cag aac taatggctac tatcgccaac	623
Ser Gly Ala Ala Gln Glu Glu Gln Asn	
195 200	

cca

626

<210> 296  
<211> 201  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 296  
Ser Val Glu Leu Pro Ala Glu Ile Phe Asp Arg Glu Val Ser Val Ala  
1 5 10 15  
Leu Leu His Gln Val Val Asn Ala Gln Leu Ala Ala Ala Arg Gln Gly  
20 25 30  
Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Gly Arg Lys  
35 40 45  
Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg  
50 55 60  
Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg  
65 70 75 80  
Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr  
85 90 95  
Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser  
100 105 110  
Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe  
115 120 125  
Ile Glu Arg Leu Thr Glu Arg Lys Ser Val Leu Leu Val Val Ser Arg  
130 135 140  
Glu Asp Ile Asn Ala Gln Lys Ser Ala Asn Asn Leu Pro Gly Val His  
145 150 155 160  
Ile Leu Ala Ala Asp Gln Leu Asn Thr Tyr Asp Val Leu Lys Ser Asp  
165 170 175  
Asp Val Val Phe Ser Val Glu Ala Leu His Thr Phe Ile Asn Arg Ala  
180 185 190  
Ser Gly Ala Ala Gln Glu Glu Gln Asn  
195 200

<210> 297  
<211> 696  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(673)  
<223> RXN00706

<400> 297  
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agaaggtccg cgtttctcgt cgcaatggga aggatatcta atg act gag aat tac 115  
Met Thr Glu Asn Tyr  
1 5

atc cct cgt ctg aag acc cgt tac cag gac gaa atc cgc acc aag ctt 163  
Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu Ile Arg Thr Lys Leu  
10 15 20

cag ggc gag ttc gag ttc gaa aac gtc atg cag atc cca ggc gtc acc 211  
Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln Ile Pro Gly Val Thr  
25 30 35

aag att gtc gtc aac atg ggt gtc ggc gac gca gct cgt gac tcc aag 259  
Lys Ile Val Val Asn Met Gly Val Gly Asp Ala Ala Arg Asp Ser Lys  
40 45 50

ctc atc aac ggc gct atc gag gac ctc acc gca atc acc ggt cag aag 307  
Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala Ile Thr Gly Gln Lys  
55 60 65

cca cag ctt cgc cgt gcg aag aag tcc atc gct aac ttc aag ctc cgt 355  
Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala Asn Phe Lys Leu Arg  
70 75 80 85

gaa ggc atg cca atc ggc gca aag gtt acc ctg cgc ggc gac cgc atg 403  
Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu Arg Gly Asp Arg Met  
90 95 100

tgg gag ttc ctg gac cgt ctg ctg acc gtg gca ctg cca cgt atc cgc 451  
Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg  
105 110 115

gac ttc cgt gga ctt tcc gac cag cag ttc gac ggc cac ggt aac tac 499  
Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr  
120 125 130

acc ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac 547  
Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp  
135 140 145

aag atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct 595  
Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala  
150 155 160 165

gta acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca 643  
Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro  
170 175 180

ttc aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaaagc 693  
Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln  
185 190

act 696

&lt;210&gt; 298

&lt;211&gt; 191

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 298

Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu  
 1 5 10 15  
 Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln  
 20 25 30  
 Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala  
 35 40 45  
 Ala Arg Asp Ser Lys Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala  
 50 55 60  
 Ile Thr Gly Gln Lys Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala  
 65 70 75 80  
 Asn Phe Lys Leu Arg Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu  
 85 90 95  
 Arg Gly Asp Arg Met Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala  
 100 105 110  
 Leu Pro Arg Ile Arg Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp  
 115 120 125  
 Gly His Gly Asn Tyr Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr  
 130 135 140  
 Glu Ile Asp Val Asp Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr  
 145 150 155 160  
 Val Val Thr Thr Ala Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg  
 165 170 175  
 Glu Leu Gly Phe Pro Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln  
 180 185 190

&lt;210&gt; 299

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(256)

&lt;223&gt; FRXA00711

&lt;400&gt; 299

tggtcatcga ctccgacgga aaccgaactc gcgttggcta ccgtttcgat gaaaacggca 60  
 agaaggtccg cgtttctcgt cgcaatggga aggatatcta atg act gag aat tac 115  
 Met Thr Glu Asn Tyr  
 1 5  
 atc cct cgt ctg aag acc cgt tac cag gac gaa atc cgc acc aag ctt 163  
 Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu Ile Arg Thr Lys Leu  
 10 15 20  
 cag ggc gag ttc gag ttc gaa aac gtc atg cag atc cca ggc gtc acc 211  
 Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln Ile Pro Gly Val Thr

25

30

35

aag att gtc gtc aac atg ggt gtc ggc gac gca gct cgt gac tcc 256  
 Lys Ile Val Val Asn Met Gly Val Gly Asp Ala Ala Arg Asp Ser  
           40                  45                  50

&lt;210&gt; 300

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 300

Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu  
   1                  5                  10                  15

Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln  
           20                  25                  30

Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala  
           35                  40                  45

Ala Arg Asp Ser  
       50

&lt;210&gt; 301

&lt;211&gt; 290

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(267)

&lt;223&gt; FRXA00706

&lt;400&gt; 301

gag ttc ctg gac cgt ctg ctg acc gtg gca ctg cca cgt atc cgc gac 48  
 Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp  
   1                  5                  10                  15

ttc cgt gga ctt tcc gac cag cag ttc gac ggc cac ggt aac tac acc 96  
 Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr  
           20                  25                  30

ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac aag 144  
 Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys  
           35                  40                  45

atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct gta 192  
 Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val  
       50                  55                  60

acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca ttc 240  
 Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe  
       65                  70                  75                  80

aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaagc 287  
 Lys Gly Glu Asp Gly Asn Arg Gln Gln  
                   85

290

<400> 302

Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp  
1 5 10 15

Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr  
20 25 30

Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys  
35 40 45

Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val  
50 55 60

Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe  
65 70 75 80

Lys Gly Glu Asp Gly Asn Arg Gln Gln  
85

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<220>
<221> CDS
<222> (101)..(634)
<223> RXA00695
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<400> 303																
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gtcctcgcct	acgtctggta	atagggagga	ttgactaaat	atg	tca	cgt	atc	gga	115							
				Met	Ser	Arg	Ile	Gly								
				1				5								
aaa	gaa	ccg	atc	acc	atc	cca	tcc	ggt	gtc	gaa	acc	aag	att	gac	gga	163
Lys	Glu	Pro	Ile	Thr	Ile	Pro	Ser	Gly	Val	Glu	Thr	Lys	Ile	Asp	Gly	
				10					15					20		
cag	ctc	gtt	gag	gtt	aag	ggt	cct	aag	ggc	acc	ctg	aac	gtt	aac	gtt	211
Gln	Leu	Val	Glu	Val	Lys	Gly	Pro	Lys	Gly	Thr	Leu	Asn	Val	Asn	Val	
			25					30					35			
cca	gag	cca	atc	tcc	gtt	gca	gtg	gaa	gac	ggc	aag	att	gtc	gtc	acc	259
Pro	Glu	Pro	Ile	Ser	Val	Ala	Val	Glu	Asp	Gly	Lys	Ile	Val	Val	Thr	
			40				45					50				
cgc	ccg	gat	gat	cac	cgc	act	aac	cgt	tcc	ctc	cac	ggg	ctc	tcc	cgc	307
Arg	Pro	Asp	Asp	His	Arg	Thr	Asn	Arg	Ser	Leu	His	Gly	Leu	Ser	Arg	
	55					60					65					

tcc ctg gtt aac aac ctg gtt gtc ggc gtc acc gag ggc tac acc atc 355  
 Ser Leu Val Asn Asn Leu Val Val Gly Val Thr Glu Gly Tyr Thr Ile  
 70 75 80 85

aag atg gaa atc ttc ggt gtc ggt tac cgt gtc gcg ctg aag ggc aag 403  
 Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val Ala Leu Lys Gly Lys  
 90 95 100

gac ctt gag ttc tcc ctc ggc tac tca cac cca gtt ctg att gaa gct 451  
 Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro Val Leu Ile Glu Ala  
 105 110 115

tct gaa ggc atc act ttc gca gtt gat ggc aac acc aag ctt tca gtt 499  
 Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn Thr Lys Leu Ser Val  
 120 125 130

tct ggc atc gac aag cag aag gtt gga cag gtc gca gca gtg atc cgc 547  
 Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val Ala Ala Val Ile Arg  
 135 140 145

cgc ctg cgt aag gac gat cct tac aag ggt aag ggc atc cgc tac gag 595  
 Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys Gly Ile Arg Tyr Glu  
 150 155 160 165

ggt gag cag atc cgc cgc aag gtc gga aag acg ggt aag taagcaatga 644  
 Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr Gly Lys  
 170 175

gcaacactga aaa 657

<210> 304

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met Ser Arg Ile Gly Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu  
 1 5 10 15

Thr Lys Ile Asp Gly Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr  
 20 25 30

Leu Asn Val Asn Val Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly  
 35 40 45

Lys Ile Val Val Thr Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu  
 50 55 60

His Gly Leu Ser Arg Ser Leu Val Asn Asn Leu Val Val Gly Val Thr  
 65 70 75 80

Glu Gly Tyr Thr Ile Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val  
 85 90 95

Ala Leu Lys Gly Lys Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro  
 100 105 110

Val Leu Ile Glu Ala Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn  
 115 120 125

Thr Lys Leu Ser Val Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val  
 130 135 140

Ala Ala Val Ile Arg Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys  
 145 150 155 160

Gly Ile Arg Tyr Glu Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr  
 165 170 175

Gly Lys

<210> 305

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA00543

<400> 305

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aacattcaca aacactcaaa aaccacgaaa ggcagggatc atg aag ctg atc ctc 115  
 Met Lys Leu Ile Leu  
 1 5

acc gcc gcc gtt gaa aac ctt ggt gtc gct ggc gac atc gta gag gtt 163  
 Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly Asp Ile Val Glu Val  
 10 15 20

aag aac ggc tac gga cgt aac ctg ctg ctc ccc cgt ggc ctg gca atc 211  
 Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro Arg Gly Leu Ala Ile  
 25 30 35

gta gcc acc ccg ggt gct gag aag cag atc gag ggc atc aag cgt gcc 259  
 Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu Gly Ile Lys Arg Ala  
 40 45 50

cag gag gct cgc gag att cgc gac ctc gac cac gct cgc gaa gtt aag 307  
 Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His Ala Arg Glu Val Lys  
 55 60 65

gta gca ctg gaa gca ctt gaa ggt gtt acc att gca gtc cgc acc tcc 355  
 Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile Ala Val Arg Thr Ser  
 70 75 80 85

gag agc gga aaa ctg ttc ggc tcc gtt aag act gac gac atc gtc gac 403  
 Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr Asp Asp Ile Val Asp  
 90 95 100

gca gtc aag gca gcc ggc ggc ccg aac ctg gac aag cgt gcc att gtt 451  
 Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp Lys Arg Ala Ile Val  
 105 110 115

ctc ccg aag aac ctg gtt aag acc acc ggt aag tac cag gta gaa gca 499  
 Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys Tyr Gln Val Glu Ala  
 120 125 130

aag ctc acc gac gga att gtt tcc gcg tgaagtttga ggtcgtcgca 546  
 Lys Leu Thr Asp Gly Ile Val Ser Ala  
 135 140

gcg 549

<210> 306  
 <211> 142  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 306  
 Met Lys Leu Ile Leu Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly  
 1 5 10 15  
 Asp Ile Val Glu Val Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro  
 20 25 30  
 Arg Gly Leu Ala Ile Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu  
 35 40 45  
 Gly Ile Lys Arg Ala Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His  
 50 55 60  
 Ala Arg Glu Val Lys Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile  
 65 70 75 80  
 Ala Val Arg Thr Ser Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr  
 85 90 95  
 Asp Asp Ile Val Asp Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp  
 100 105 110  
 Lys Arg Ala Ile Val Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys  
 115 120 125  
 Tyr Gln Val Glu Ala Lys Leu Thr Asp Gly Ile Val Ser Ala  
 130 135 140

<210> 307  
 <211> 636  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> RXA01335

<400> 307  
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 cggatcagta gattacacat aagaggaagg aggcgaagta atg gca aac cca aga 115  
 Met Ala Asn Pro Arg  
 1 5  
 aac gaa gca gct ctg gca gag ctc aag gca cgt ttc gct gag acc gac 163  
 Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg Phe Ala Glu Thr Asp

10										15					20					
acc gtc gtt ctc acc gag tac cgt ggc ctg acc gtg gct cag acc acc	211																			
Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr Val Ala Gln Thr Thr																				
25 30 35																				
gaa ctg cgt aag gca ctg ggc ttc gat gtc cag tac tcc gtc gcc aag	259																			
Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln Tyr Ser Val Ala Lys																				
40 45 50																				
aac acc ctt gtt aag atc gcc gct aac gaa gct ggc gtc gag ggc ctt	307																			
Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala Gly Val Glu Gly Leu																				
55 60 65																				
gat gat ctc ctg acc ggt cca acc gct gtt gcc ttc atc aag ggc gaa	355																			
Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala Phe Ile Lys Gly Glu																				
70 75 80 85																				
gca gtt gac acc gct aag gtg ctg aag aaa ttc ggc gaa gaa aac aag	403																			
Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe Gly Glu Glu Asn Lys																				
90 95 100																				
gca ttc gta gtc aag ggt ggc tac atg gat ggc aac gcg ctg acc gct	451																			
Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly Asn Ala Leu Thr Ala																				
105 110 115																				
gaa cag gtc aac gca atc gcc gag ctg gac aac cgt gag acc act ctc	499																			
Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn Arg Glu Thr Thr Leu																				
120 125 130																				
gcg aag ctt gcc ggc gcc atg aag ggc agc ttg gca aag gcc gca ggc	547																			
Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu Ala Lys Ala Ala Gly																				
135 140 145																				
ctg ttc aac gct cct gct tcc cag gtc gca cgc ctc gcc gtt gcg ctc	595																			
Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg Leu Ala Val Ala Leu																				
150 155 160 165																				
cag gac aag aag gac gca taagtcgccca ccaggcgccac cag	636																			
Gln Asp Lys Lys Asp Ala																				
170																				

&lt;210&gt; 308

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 308

Met Ala Asn Pro Arg Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg	
1 5 10 15	
Phe Ala Glu Thr Asp Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr	
20 25 30	
Val Ala Gln Thr Thr Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln	
35 40 45	
Tyr Ser Val Ala Lys Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala	
50 55 60	



Gly Val Glu Gly Leu Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala  
 65 70 75 80  
 Phe Ile Lys Gly Glu Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe  
 85 90 95  
 Gly Glu Glu Asn Lys Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly  
 100 105 110  
 Asn Ala Leu Thr Ala Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn  
 115 120 125  
 Arg Glu Thr Thr Leu Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu  
 130 135 140  
 Ala Lys Ala Ala Gly Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg  
 145 150 155 160  
 Leu Ala Val Ala Leu Gln Asp Lys Lys Asp Ala  
 165 170

<210> 309  
 <211> 558  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(535)  
 <223> RXN02826

<400> 309  
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 Met Ala Pro Lys Lys  
 1 5  
 aag aag aag gtc act ggc ctc atc aag ctc cag atc cag gca gga cag 163  
 Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln Ile Gln Ala Gly Gln  
 10 15 20  
 gca aac cct gct cct cca gtt ggc cca gca ctt ggt gct cac ggc gtc 211  
 Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu Gly Ala His Gly Val  
 25 30 35  
 aac atc atg gaa ttc tgc aag gct tac aac gct gcg act gaa aac cag 259  
 Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala Ala Thr Glu Asn Gln  
 40 45 50  
 cgc ggc aac gtt gtt cct gtt gag atc acc gtt tac gaa gac cgt tca 307  
 Arg Gly Asn Val Val Pro Val Glu Ile Thr Val Tyr Glu Asp Arg Ser  
 55 60 65  
 ttc gac ttc aag ctg aag act cct cca gct gca aag ctt ctt ctg aag 355  
 Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala Lys Leu Leu Leu Lys  
 70 75 80 85  
 gct gct ggc ctg cag aag ggc tcc ggc gtt cct cac acc cag aag gtc 403  
 Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro His Thr Gln Lys Val

90 95 100

ggc aag gtt tcc atg gct cag gtt cgt gag atc gct gag acc aag aag 451  
Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile Ala Glu Thr Lys Lys  
105 110 115

gaa gac ctg aac gct cgc gat atc gac gct gct gcg aag atc atc gct 499  
Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala Ala Lys Ile Ile Ala  
120 125 130

ggt acc gct cgt tcc atg ggc atc acc gtc gaa ggc taaaagcttt 545  
Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu Gly  
135 140 145

cacaccggtt agt 558

<210> 310  
<211> 145  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 310  
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Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala  
35 40 45  
Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val  
50 55 60  
Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala  
65 70 75 80  
Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro  
85 90 95  
His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile  
100 105 110  
Ala Glu Thr Lys Lys Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala  
115 120 125  
Ala Lys Ile Ile Ala Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu  
130 135 140  
Gly  
145

<210> 311  
<211> 465  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS

&lt;222&gt; (67)..(465)

&lt;223&gt; FRXA02826

&lt;400&gt; 311

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ttaacg atg gct cct aag aag aag aag aag gtc act ggc ctc atc aag 108  
Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys  
1 5 10

ctc cag atc cag gca gga cag gca aac cct gct cct cca gtt ggc cca 156  
Leu Gln Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro  
15 20 25 30

gaa ctt ggt gct cac ggc gtc aac atc atg gaa ttc tgc aag gct tac 204  
Glu Leu Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr  
35 40 45

aac gct gcg act gaa aac cag cgc ggg aac gtt gtt cct gtt gag atc 252  
Asn Ala Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile  
50 55 60

acc gtt tac gaa gac cgt tca ttc gac ttc aag ctg aag act cct cca 300  
Thr Val Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro  
65 70 75

gct gca aag ctt ctt ctg aaa gct gct ggc ctg cag aag ggc tcc ggc 348  
Ala Ala Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly  
80 85 90

gtt cct cac acc cag aag gtc ggc aag gtt tcc atg gct cag gtt cgt 396  
Val Pro His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg  
95 100 105 110

gag atc cct gcg acc aag aac gaa gac ctg acg ctc gcg ata tcg acg 444  
Glu Ile Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr  
115 120 125

ctg ctg cga aga tca tcg ctg 465  
Leu Leu Arg Arg Ser Ser Leu  
130

&lt;210&gt; 312

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 312

Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln  
1 5 10 15

Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu Leu  
20 25 30

Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala  
35 40 45

Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val  
50 55 60

Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala  
 65 70 75 80  
 Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro  
 85 90 95  
 His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile  
 100 105 110  
 Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu Leu  
 115 120 125  
 Arg Arg Ser Ser Leu  
 130

&lt;210&gt; 313

&lt;211&gt; 507

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(484)

&lt;223&gt; RXA01334

&lt;400&gt; 313

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 Met Ala Lys Leu Thr  
 1 5  
 aaa gac gag ctc atc gag gct ttc aag gaa atg acc ctc atc gag ctc 163  
 Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met Thr Leu Ile Glu Leu  
 10 15 20  
 tcc gag ttc gtt aag gaa ttc gaa gag gtc ttc gac gta acc gca gct 211  
 Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe Asp Val Thr Ala Ala  
 25 30 35  
 gct cca gtt gca gtt gct gct gca ggc gct gca ggc ggc gaa gct gct 259  
 Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala Gly Gly Glu Ala Ala  
 40 45 50  
 gct gca gaa gag aag gac gag ttc gac gtc gtt ctc gaa gac gca ggc 307  
 Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val Leu Glu Asp Ala Gly  
 55 60 65  
 gca aag aag atc ggc gtc atc aag gct gtc cgc gag ctc gtc tcc ggc 355  
 Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg Glu Leu Val Ser Gly  
 70 75 80 85  
 ctg ggc ctg aag gaa gca aag gag ctc gtt gag ggc gca cct aag gct 403  
 Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Gly Ala Pro Lys Ala  
 90 95 100  
 atc ctc gag ggc gca aac aag gac gac gct gag gct gca aag gct aag 451  
 Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu Ala Ala Lys Ala Lys  
 105 110 115

ctc gaa gag gct ggc gca aag gtc acc ctt aag taagaacttt cttacacctt 504  
Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys  
120 125

ttc

507

&lt;210&gt; 314

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 314

Met Ala Lys Leu Thr Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met  
1 5 10 15

Thr Leu Ile Glu Leu Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe  
20 25 30

Asp Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Gly Ala Ala  
35 40 45

Gly Gly Glu Ala Ala Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val  
50 55 60

Leu Glu Asp Ala Gly Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg  
65 70 75 80

Glu Leu Val Ser Gly Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu  
85 90 95

Gly Ala Pro Lys Ala Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu  
100 105 110

Ala Ala Lys Ala Lys Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys  
115 120 125

&lt;210&gt; 315

&lt;211&gt; 353

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(330)

&lt;223&gt; RXA02037

&lt;400&gt; 315

ggc aag ggc aag cct ttg tac gca cct aac gtt gac tgc ggc gac cac 48  
Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His  
1 5 10 15

gta atc gtg atc aac gct gac aag gtt gca gtt acc tcc aac aag cgc 96  
Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg  
20 25 30

gag cgc gaa atg cgt tac cgc cac tcc ggt tac cct ggt ggc ctg aag 144

Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys  
35 40 45  
tcc atg acc ctg ggt cgt tcc ctg gat ctg cac cca gag cgc acc atc 192  
Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile  
50 55 60  
gag gat tcc atc gtc ggc atg atg cca cac aac aag ctc act gct gct 240  
Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala  
65 70 75 80  
tcc gca aag aag ctg cac gtt ttc tcc ggc tcc gag cac cca tac gct 288  
Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala  
85 90 95  
gct cag aag cct gag gcc tac gag atc aag aag gtg gcc cag 330  
Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln  
100 105 110  
taatgtcaga gcctatccag aac 353

<210> 316  
<211> 110  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 316  
Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His  
1 5 10 15  
Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg  
20 25 30  
Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys  
35 40 45  
Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile  
50 55 60  
Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala  
65 70 75 80  
Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala  
85 90 95  
Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln  
100 105 110

<210> 317  
<211> 567  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(544)  
<223> RXA00699

<400> 317

ccacaccgtg atccgccccg ataccccaga ggtacgtggc atgacctgg cagttcgcca 60  
cctgatcgtc gtcgaagaag tggcggggga gtaggtaaca atg agc gaa cca att 115  
Met Ser Glu Pro Ile  
1 5  
aag ctc cac gat ttg cgc cca gca gcg ggc tca aac aaa gct aag acc 163  
Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser Asn Lys Ala Lys Thr  
10 15 20  
cgc gtt ggt cga ggc gaa gca tcc aag ggt aag act gca ggt cgc ggt 211  
Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys Thr Ala Gly Arg Gly  
25 30 35  
acc aag ggt acc aag gca cgc aag cag gtt tct gca gca ttc gaa ggt 259  
Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser Ala Ala Phe Glu Gly  
40 45 50  
ggc cag atg cca ctg cag atg cgt ctt cct aag ctg aag ggc ttc aag 307  
Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys Leu Lys Gly Phe Lys  
55 60 65  
aac cct aac aag gtt gac tac cag gta gtt aac att gca gat ctc gca 355  
Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn Ile Ala Asp Leu Ala  
70 75 80 85  
gag aag ttc cca cag ggc ggc gac gtc agc att gct gac atc gtt gca 403  
Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile Ala Asp Ile Val Ala  
90 95 100  
gca gga ctt gtc cgc aag aac gaa ctg gtt aag gtt ctt ggc aac ggc 451  
Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys Val Leu Gly Asn Gly  
105 110 115  
gac atc agc gtc aag ctg aac gtc acc gct aac aag ttc tcc ggc tct 499  
Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn Lys Phe Ser Gly Ser  
120 125 130  
gcc aag gaa aag atc gaa gcc gct ggc ggc tcc gca acc gtg gca 544  
Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser Ala Thr Val Ala  
135 140 145  
taagttcacc agaactttaaa aaa 567

&lt;210&gt; 318

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 318

Met Ser Glu Pro Ile Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser  
1 5 10 15

Asn Lys Ala Lys Thr Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys  
20 25 30

Thr Ala Gly Arg Gly Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser  
35 40 45

Ala Ala Phe Glu Gly Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys

<400> 319																
atgcacccgc agagcgcgcgc gcccgcggcgc accgcaacgc acgtccgcgt cgtggtggcc																60
agcgtcgtca gcgtgctgag cagaagcagg agggctaacc																
<div> <div>atg</div> <div>Met</div> <div>1</div> </div> <div> <div>ctt</div> <div>Leu</div> <div>5</div> </div> <div> <div>att</div> <div>Ile</div> <div>10</div> </div> <div> <div>cct</div> <div>Pro</div> <div>15</div> </div> <div> <div>aag</div> <div>Lys</div> <div>20</div> </div>																115
cgc gtt aag tac cgt cgc cag cac cgt cct acc cgt agt ggt atc tcc																163
<div>Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr Arg Ser Gly Ile Ser</div> <div>10 15 20</div>																
aag ggc ggc aac cgc gtc act ttc ggt gag tac ggc atc cag gct ctc																211
<div>Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr Gly Ile Gln Ala Leu</div> <div>25 30 35</div>																
gag cct gcc tac atc acc aac cgt cag att gaa tct gca cgt att gca																259
<div>Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu Ser Ala Arg Ile Ala</div> <div>40 45 50</div>																
atc aac cgc cac gtc agg cgt ggt ggc aag gtt tgg atc aac atc ttc																307
<div>Ile Asn Arg His Val Arg Arg Gly Gly Lys Val Trp Ile Asn Ile Phe</div> <div>55 60 65</div>																
cca gac cgc cca ctg acc cag aag cca ctc ggc gtt cgt atg ggt tcc																355
<div>Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly Val Arg Met Gly Ser</div> <div>70 75 80 85</div>																
ggt aag ggc cct gtg gag aag tgg gtt gca aac atc aag ccg ggc cgt																403
<div>Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn Ile Lys Pro Gly Arg</div> <div>90 95 100</div>																



atc ctc ttc gag atg agc tac ccg gac gaa gct act gct ctc gag gct 451  
Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala Thr Ala Leu Glu Ala  
105 110 115

ctg cgc cgc gct ggc cag aag ctt cca tgc aag gtc cgt atc gtc aag 499  
Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys Val Arg Ile Val Lys  
120 125 130

agg gag gat cag ctc taatggctat cggtacccca gca 537  
Arg Glu Asp Gln Leu  
135

<210> 320

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Leu Ile Pro Lys Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr  
1 5 10 15

Arg Ser Gly Ile Ser Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr  
20 25 30

Gly Ile Gln Ala Leu Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu  
35 40 45

Ser Ala Arg Ile Ala Ile Asn Arg His Val Arg Arg Gly Gly Lys Val  
50 55 60

Trp Ile Asn Ile Phe Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly  
65 70 75 80

Val Arg Met Gly Ser Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn  
85 90 95

Ile Lys Pro Gly Arg Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala  
100 105 110

Thr Ala Leu Glu Ala Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys  
115 120 125

Val Arg Ile Val Lys Arg Glu Asp Gln Leu  
130 135

<210> 321

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA00670

<400> 321

gaaactggtg gctacatcga tgtcgaggcg gaagattccg agtaagtcgc atggtccaat 60

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<400> 322
Met  Pro  Thr  Pro  Lys  Lys  Gly  Ala  Arg  Leu  Gly  Gly  Ser  Ala  Ser  His
   1              5              10              15

Gln  Lys  Lys  Ile  Leu  Ser  Asn  Leu  Ala  Ala  Ser  Leu  Phe  Glu  His  Gly
           20              25              30

Ala  Ile  Lys  Thr  Thr  Asp  Ala  Lys  Ala  Lys  Ala  Leu  Arg  Pro  Tyr  Ala
      35              40              45

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Glu Lys Leu Ile Thr Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg  
50 55 60

Asn Val Leu Ala Leu Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe  
65 70 75 80

Asn Glu Leu Ala Pro Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg  
85 90 95

Ile Ile Lys Leu Glu Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln  
100 105 110

Ile Ser Leu Val Leu Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala  
115 120 125

Thr Arg Ala Ser Ala Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu  
130 135 140

Glu Val Val Glu Ala Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala  
145 150 155 160

Glu Glu Lys

<210> 323

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA00696

<400> 323

gatccgccgc ctgcgtaagg acgatcctta caagggttaag ggcacccgct acgaggggtga 60

gcagatccgc cgcaagggtcg gaaagacggg taagtaagca atg agc aac act gaa 115  
Met Ser Asn Thr Glu  
1 5

aac aag cag aag cgc gtt tcc gtt ggc aag gac atc gcg act cgt cgt 163  
Asn Lys Gln Lys Arg Val Ser Val Gly Lys Asp Ile Ala Thr Arg Arg  
10 15 20

cgc gtt gcc cgt gca cgc cgc cac ttc cgc atc cgc aag aac ctg cgt 211  
Arg Val Ala Arg Ala Arg Arg His Phe Arg Ile Arg Lys Asn Leu Arg  
25 30 35

ggc acc cca gag gct cca cgt ttg gtt gtc cac cgc tct tct cgc cac 259  
Gly Thr Pro Glu Ala Pro Arg Leu Val Val His Arg Ser Ser Arg His  
40 45 50

atg cac gtt cag atc atc gat gac gtt gca ggc cac acc ctg gct gca 307  
Met His Val Gln Ile Ile Asp Asp Val Ala Gly His Thr Leu Ala Ala  
55 60 65

gct tct tcc atc gag gct gag gtt cgc gca act gag ggc gac aag aag 355  
Ala Ser Ser Ile Glu Ala Glu Val Arg Ala Thr Glu Gly Asp Lys Lys

70                      75                      80                      85

gct aag ggc gca aag gtc ggt cag ctg atc gcc gag cgc gct aag gct 403  
Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala Glu Arg Ala Lys Ala  
                    90                      95                      100

gct ggt atc gag cag gtc gtc ttc gac cgc gct ggt tac aag tac cac 451  
Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala Gly Tyr Lys Tyr His  
                    105                      110                      115

ggc cgc gtt gca gct ctc gct gac gcc gct cgt gaa ggt ggt ctg aaa 499  
Gly Arg Val Ala Ala Leu Ala Asp Ala Ala Arg Glu Gly Gly Leu Lys  
                    120                      125                      130

ttc taatgatgac catttctaag aac 525  
Phe

<210> 324  
<211> 134  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 324  
Met Ser Asn Thr Glu Asn Lys Gln Lys Arg Val Ser Val Gly Lys Asp  
1                      5                      10                      15

Ile Ala Thr Arg Arg Arg Val Ala Arg Ala Arg Arg His Phe Arg Ile  
                    20                      25                      30

Arg Lys Asn Leu Arg Gly Thr Pro Glu Ala Pro Arg Leu Val Val His  
                    35                      40                      45

Arg Ser Ser Arg His Met His Val Gln Ile Ile Asp Asp Val Ala Gly  
50                      55                      60

His Thr Leu Ala Ala Ala Ser Ser Ile Glu Ala Glu Val Arg Ala Thr  
65                      70                      75                      80

Glu Gly Asp Lys Lys Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala  
                    85                      90                      95

Glu Arg Ala Lys Ala Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala  
100                      105                      110

Gly Tyr Lys Tyr His Gly Arg Val Ala Ala Leu Ala Asp Ala Ala Arg  
115                      120                      125

Glu Gly Gly Leu Lys Phe  
130

<210> 325  
<211> 462  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(439)

&lt;223&gt; RXA01353

&lt;400&gt; 325

cagcctcgaa aattgaaacg gaaacgaacc ggccgagcac cccaaacctg gggaagtgcc 60

gccagggtcc tctttcccta ctagtaaaag gattgtttat atg aac att ctg gat 115  
 Met Asn Ile Leu Asp  
 1 5

aag atc gac gca gca tcc ctg cgc gac gac gtt cct gca ttc cgc gcc 163  
 Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val Pro Ala Phe Arg Ala  
 10 15 20

ggc gac acc ctc gac gta cac gtc aag gtc atc gaa ggc acc acc acc 211  
 Gly Asp Thr Leu Asp Val His Val Lys Val Ile Glu Gly Thr Thr Thr  
 25 30 35

cgt acc cag ctg ttc aag ggt gtt gtc att cgc cgt cag ggc ggc gga 259  
 Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg Arg Gln Gly Gly Gly  
 40 45 50

atc cgc gag acc ttc acc gta cgt aag gtt tcc ttc ggc atc ggt gtt 307  
 Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser Phe Gly Ile Gly Val  
 55 60 65

gag cgt acc ttc cca gta cac tcc cca aac atc gag aag atc gag gtc 355  
 Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile Glu Lys Ile Glu Val  
 70 75 80 85

att cgt cgt ggt gac gtt cgt cgt gcg aag ctg tac tac ctg cgc gaa 403  
 Ile Arg Arg Gly Asp Val Arg Arg Ala Lys Leu Tyr Tyr Leu Arg Glu  
 90 95 100

ctg cgc ggc aag gct gca cgt att aag gag aag cgc taattattta 449  
 Leu Arg Gly Lys Ala Ala Arg Ile Lys Glu Lys Arg  
 105 110

gcgtttgtta ggt 462

&lt;210&gt; 326

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 326

Met Asn Ile Leu Asp Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val  
 1 5 10 15

Pro Ala Phe Arg Ala Gly Asp Thr Leu Asp Val His Val Lys Val Ile  
 20 25 30

Glu Gly Thr Thr Thr Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg  
 35 40 45

Arg Gln Gly Gly Gly Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser  
 50 55 60

Phe Gly Ile Gly Val Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile  
 65 70 75 80

<400> 327																
cgacaccaag cgcatgaagc gcctgctcgg caaggcttaa gtttaaaacc ttgcgctaaa																60
cccctccacc tttcaagaca agattttaagg aagtaccacc																115
Val Ala Arg Val Lys																5
cgg tcc gtt aac gca aag aag aag cgt cgc gaa att ctg aag tcc gca																163
Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu Ile Leu Lys Ser Ala																20
aag ggc tac cgc ggc cag cgc tca cgc ctt tac cgt aag gct aag gag																211
Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr Arg Lys Ala Lys Glu																35
cag tgg ctg cac tcc atg act tac tct tac cgc gat cgt cgc gcc cgt																259
Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg Asp Arg Arg Ala Arg																40
aag agc gag ttc cgt aag ctg tgg atc cag cgt atc aac gct gct gca																307
Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg Ile Asn Ala Ala Ala																55
cgt atg aac ggc atc acc tac aac cgt ctc atc cag ggc ctt cgc ctt																355
Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile Gln Gly Leu Arg Leu																70
gct gag atc gag gtc gac cgc aag atc ctc gct gat ctc gca gtc aac																403
Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala Asp Leu Ala Val Asn																90
gac ttt gca acc ttc tcc gca atc tgc gag gct gca aag gct gca ctt																451
Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala Ala Lys Ala Ala Leu																105
cct gag gac gtt aac gct cca aag gct gct taagcttaca aacgaattga																501
Pro Glu Asp Val Asn Ala Pro Lys Ala Ala																120
cct																504

<210> 328  
 <211> 127  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 328  
 Val Ala Arg Val Lys Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu  
           1                  5                  10                  15  
 Ile Leu Lys Ser Ala Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr  
                   20                  25                  30  
 Arg Lys Ala Lys Glu Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg  
           35                  40                  45  
 Asp Arg Arg Ala Arg Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg  
           50                  55                  60  
 Ile Asn Ala Ala Ala Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile  
           65                  70                  75                  80  
 Gln Gly Leu Arg Leu Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala  
                   85                  90                  95  
 Asp Leu Ala Val Asn Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala  
           100                  105                  110  
 Ala Lys Ala Ala Leu Pro Glu Asp Val Asn Ala Pro Lys Ala Ala  
           115                  120                  125

<210> 329  
 <211> 415  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(415)  
 <223> RXN02371

<400> 329  
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 cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115  
   Met Tyr Ala Ile Val  
   1                  5  
 aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163  
 Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys  
                   10                  15                  20  
 gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211  
 Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro  
           25                  30                  35  
 gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259  
 Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu  
           40                  45                  50

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gta agc cct cgg                                415
Val Ser Pro Arg
105
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<400> 330
Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu
  1          5          10          15
Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser
          20          25          30
Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr
          35          40          45
Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu
          50          55          60
His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr
  65          70          75          80
Gly Tyr Lys Lys Arg Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys
          85          90          95
Val Thr Gly Asn Gln Val Ser Pro Arg
          100          105

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<400> 331
ttggctccgc atgtctaaaa cgcaattgta aaacgtaagt ccaatcaggg actcatcatc 60

cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115
               Met Tyr Ala Ile Val
                   1           5

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aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163  
Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys  
10 15 20  
gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211  
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro  
25 30 35  
gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259  
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu  
40 45 50  
gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307  
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro  
55 60 65  
aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355  
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg  
70 75 80 85  
cag gga cac cgt cag 370  
Gln Gly His Arg Gln  
90

<210> 332  
<211> 90  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 332  
Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu  
1 5 10 15  
Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser  
20 25 30  
Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr  
35 40 45  
Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu  
50 55 60  
His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr  
65 70 75 80  
Gly Tyr Lys Lys Arg Gln Gly His Arg Gln  
85 90

<210> 333  
<211> 426  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(403)  
<223> RXA01949

&lt;400&gt; 333

cctacgacgt tctcaagtct gacgacgttg tgtttctccgt tgaggctctc cacaccttca 60  
tcaaccgcgc ttccggtgcg gcacaggagg agcagaacta atg gct act atc gcc 115  
Met Ala Thr Ile Ala  
1 5  
aac cca cgc gac atc atc atc gca ccg gtc gtt tct gag aag tcc tac 163  
Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val Ser Glu Lys Ser Tyr  
10 15 20  
ggc ctc atg gag cag aac gtt tac acg ttc ttc gtc tcc act gac gct 211  
Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe Val Ser Thr Asp Ala  
25 30 35  
aac aag act cag atc aag att gcc atc gaa gag atc ttc ggc gtc aag 259  
Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu Ile Phe Gly Val Lys  
40 45 50  
gtt gca tct gtg aac acc gtt aac cgt gca ggt aag cgc aag cgc tcc 307  
Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly Lys Arg Lys Arg Ser  
55 60 65  
cgc acc ggc ttc ggt act cgc aag gct acc aag cgc gct tat gtg act 355  
Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys Arg Ala Tyr Val Thr  
70 75 80 85  
ctt cgc gaa ggc agc gac tcc atc gac atc ttc agc ggc tcc gtc gct 403  
Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe Ser Gly Ser Val Ala  
90 95 100  
taagacgtcg atagaaaagg aca 426

&lt;210&gt; 334

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 334

Met Ala Thr Ile Ala Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val  
1 5 10 15  
Ser Glu Lys Ser Tyr Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe  
20 25 30  
Val Ser Thr Asp Ala Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu  
35 40 45  
Ile Phe Gly Val Lys Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly  
50 55 60  
Lys Arg Lys Arg Ser Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys  
65 70 75 80  
Arg Ala Tyr Val Thr Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe  
85 90 95  
Ser Gly Ser Val Ala  
100



20	25	30
Ala Gly Ile Gly Asp Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro		
35	40	45
Gly Gly Asn Val Lys Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg		
50	55	60
Thr Lys Lys Glu Thr Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp		
65	70	75
Glu Asn Ala Ala Val Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr		
85	90	95
Arg Ile Phe Gly Pro Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met		
100	105	110
Lys Ile Val Ser Leu Ala Pro Glu Val Ile		
115	120	

&lt;210&gt; 337

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(339)

&lt;223&gt; FRXA00709

&lt;400&gt; 337

gtc gcc gac aac act ggt gca cgt gaa att ctg tgc atc cgc gtt ctc	48
Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys Ile Arg Val Leu	
1 5 10 15	
ggt gga tcc acc cga cgt ttt gct ggc att ggt gac gtc atc gtc gcc	96
Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala	
20 25 30	
act gtc aag gaa gca acc cca ggc ggc aac gta aag tct ggc gaa atc	144
Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile	
35 40 45	
gtc aag gct gtt atc gtt cgc acc aag aag gag acc cgt cgt gca gac	192
Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp	
50 55 60	
ggt tct tac atc tcc ttc gat gag aac gct gcc gtc atc atc aag aac	240
Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val Ile Ile Lys Asn	
65 70 75 80	
gac aac gag cca cgt ggc acc cgt atc ttc gga cca gtt gct cgt gaa	288
Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu	
85 90 95	
ctt cgt gag aag aag ttc atg aag atc gtt tct ctc gca ccg gag gtg	336
Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val	
100 105 110	
att taagaatgaa ggtccacaag ggc	362

Ile

&lt;210&gt; 338

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 338

Val	Ala	Asp	Asn	Thr	Gly	Ala	Arg	Glu	Ile	Leu	Cys	Ile	Arg	Val	Leu
1				5					10					15	

Gly	Gly	Ser	Thr	Arg	Arg	Phe	Ala	Gly	Ile	Gly	Asp	Val	Ile	Val	Ala
			20					25					30		

Thr	Val	Lys	Glu	Ala	Thr	Pro	Gly	Gly	Asn	Val	Lys	Ser	Gly	Glu	Ile
		35					40					45			

Val	Lys	Ala	Val	Ile	Val	Arg	Thr	Lys	Lys	Glu	Thr	Arg	Arg	Ala	Asp
	50					55					60				

Gly	Ser	Tyr	Ile	Ser	Phe	Asp	Glu	Asn	Ala	Ala	Val	Ile	Ile	Lys	Asn
65					70					75					80

Asp	Asn	Glu	Pro	Arg	Gly	Thr	Arg	Ile	Phe	Gly	Pro	Val	Ala	Arg	Glu
				85					90					95	

Leu	Arg	Glu	Lys	Lys	Phe	Met	Lys	Ile	Val	Ser	Leu	Ala	Pro	Glu	Val
			100					105					110		

Ile

&lt;210&gt; 339

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(412)

&lt;223&gt; RXA00710

&lt;400&gt; 339

acgagccacg tggcaccggt atcttcggac cagttgctcg tgaacttcgt gagaagaagt 60

tcatgaagat	cgtttctctc	gcaccggagg	tgatttaaga	atg	aag	gtc	cac	aag							115
				Met	Lys	Val	His	Lys							
					1			5							

ggc	gat	atg	gtt	ctg	gtc	atc	tca	ggt	cca	gac	aag	ggt	gct	aag	gga	163
Gly	Asp	Met	Val	Leu	Val	Ile	Ser	Gly	Pro	Asp	Lys	Gly	Ala	Lys	Gly	
			10					15					20			

cag	gtc	atc	gcg	gct	ttc	cct	aag	acc	gaa	aag	gtt	ctc	gtc	gaa	ggc	211
Gln	Val	Ile	Ala	Ala	Phe	Pro	Lys	Thr	Glu	Lys	Val	Leu	Val	Glu	Gly	
		25					30					35				

gtt	aac	cgc	atc	aag	aag	cac	gta	gct	aac	tcc	gca	cca	gag	cgt	ggc	259
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Val Asn Arg Ile Lys Lys His Val Ala Asn Ser Ala Pro Glu Arg Gly  
 40 45 50

gca gag tcc ggc gga atc gtg acc cag gaa gct ccg atc cat gtc tct 307  
 Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala Pro Ile His Val Ser  
 55 60 65

aac gtc atg gtc atc gac tcc gac gga aac cca act cgc gtt ggc tac 355  
 Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro Thr Arg Val Gly Tyr  
 70 75 80 85

cgt ttc gat gaa aac ggc aag aag gtc cgc gtt tct cgt cgc aat ggg 403  
 Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val Ser Arg Arg Asn Gly  
 90 95 100

aag gat atc taatgactga gaattacatc cct 435  
 Lys Asp Ile

<210> 340  
 <211> 104  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 340  
 Met Lys Val His Lys Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp  
 1 5 10 15

Lys Gly Ala Lys Gly Gln Val Ile Ala Ala Phe Pro Lys Thr Glu Lys  
 20 25 30

Val Leu Val Glu Gly Val Asn Arg Ile Lys Lys His Val Ala Asn Ser  
 35 40 45

Ala Pro Glu Arg Gly Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala  
 50 55 60

Pro Ile His Val Ser Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro  
 65 70 75 80

Thr Arg Val Gly Tyr Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val  
 85 90 95

Ser Arg Arg Asn Gly Lys Asp Ile  
 100

<210> 341  
 <211> 357  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(334)  
 <223> RXA02635

<400> 341  
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gtcttctaac tgaatgtggg cggctaggag aaagtaagtt atg tcg gca cat tgc 115
                               Met Ser Ala His Cys
                               1                               5

cag gta acg gga cgc aag ccg agt ttc ggc aag tct gtc tca cac tcg 163
Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys Ser Val Ser His Ser
                               10                               15                               20

cac cga cgc act tcc cgc cgt tgg aac ccc aac gtg cag cgt cgc aag 211
His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn Val Gln Arg Arg Lys
                               25                               30                               35

ttc tat gtc cct tcc gag gga cgc acc atc act ctg acc gtt tcc acc 259
Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr Leu Thr Val Ser Thr
                               40                               45                               50

aag ggt ctg aag gtc att gac cgc gac ggc atc gaa gcc gtt gtt gct 307
Lys Gly Leu Lys Val Ile Asp Arg Asp Gly Ile Glu Ala Val Val Ala
                               55                               60                               65

cag att cgc gca cgt ggg gag aag atc taaagatggc acgtaatgat 354
Gln Ile Arg Ala Arg Gly Glu Lys Ile
                               70                               75

atc 357

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&lt;210&gt; 342

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 342

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Met Ser Ala His Cys Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys
 1                               5                               10                               15

Ser Val Ser His Ser His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn
                20                               25                               30

Val Gln Arg Arg Lys Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr
                35                               40                               45

Leu Thr Val Ser Thr Lys Gly Leu Lys Val Ile Asp Arg Asp Gly Ile
 50                               55                               60

Glu Ala Val Val Ala Gln Ile Arg Ala Arg Gly Glu Lys Ile
 65                               70                               75

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&lt;210&gt; 343

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(241)

&lt;223&gt; RXA02043

&lt;400&gt; 343

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tgagctaccc ggacgaagct actgctctcg aggctctgcg ccgcgctggc cagaagcttc 60

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catgcaaggt ccgtatcgtc aagagggagg atcagctcta atg gct atc ggt acc 115  
 Met Ala Ile Gly Thr  
 1 5

cca gca cac gag ttc cgt gag ctc aac gag gaa gaa ctg gtt acc cgc 163  
 Pro Ala His Glu Phe Arg Glu Leu Asn Glu Glu Glu Leu Val Thr Arg  
 10 15 20

ctc aac gag gct aag gaa gaa ctg ttc aac ctt cgc ttc cag ctt gcc 211  
 Leu Asn Glu Ala Lys Glu Glu Leu Phe Asn Leu Arg Phe Gln Leu Ala  
 25 30 35

acc ggc cag ctg acc aac aac cgc cgc ctg 241  
 Thr Gly Gln Leu Thr Asn Asn Arg Arg Leu  
 40 45

<210> 344

<211> 47

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ala Ile Gly Thr Pro Ala His Glu Phe Arg Glu Leu Asn Glu Glu  
 1 5 10 15

Glu Leu Val Thr Arg Leu Asn Glu Ala Lys Glu Glu Leu Phe Asn Leu  
 20 25 30

Arg Phe Gln Leu Ala Thr Gly Gln Leu Thr Asn Asn Arg Arg Leu  
 35 40 45

<210> 345

<211> 306

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(283)

<223> RXA00698

<400> 345

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acgtattctg cgtgcacgcg caggtcagga ggcgtaagaa atg gcg ctg aag att 115  
 Met Ala Leu Lys Ile  
 1 5

act cag atc aaa ggc act gtg ggc acc aag ccc aag cat cgc gaa aat 163  
 Thr Gln Ile Lys Gly Thr Val Gly Thr Lys Pro Lys His Arg Glu Asn  
 10 15 20

ctt cgt tcc ctc ggt ctg aag cga atc cgc cac acc gtg atc cgc ccc 211  
 Leu Arg Ser Leu Gly Leu Lys Arg Ile Arg His Thr Val Ile Arg Pro  
 25 30 35

gat acc cca gag gta cgt ggc atg atc ctg gca gtt cgc cac ctg atc 259  
 Asp Thr Pro Glu Val Arg Gly Met Ile Leu Ala Val Arg His Leu Ile



40

45

50

gtc gtc gaa gaa gtg gcg ggg gag taggtaacaa tgagcgaacc aat 306  
Val Val Glu Glu Val Ala Gly Glu  
55 60

&lt;210&gt; 346

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 346

Met Ala Leu Lys Ile Thr Gln Ile Lys Gly Thr Val Gly Thr Lys Pro  
1 5 10 15

Lys His Arg Glu Asn Leu Arg Ser Leu Gly Leu Lys Arg Ile Arg His  
20 25 30

Thr Val Ile Arg Pro Asp Thr Pro Glu Val Arg Gly Met Ile Leu Ala  
35 40 45

Val Arg His Leu Ile Val Val Glu Glu Val Ala Gly Glu  
50 55 60

&lt;210&gt; 347

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(364)

&lt;223&gt; RXA02633

&lt;400&gt; 347

ccaaatcatg gtgatgcata cttaccgaac ccaactcggg cacgatctgg catccgctgg 60

aaccgacctg aagtttcaat cctgagggaa tcgagagtaa atg aaa aag gat atc 115  
Met Lys Lys Asp Ile  
1 5

cac cct gac tac cat gcg gta gtc ttc cag gac gca ggt act ggc ttc 163  
His Pro Asp Tyr His Ala Val Val Phe Gln Asp Ala Gly Thr Gly Phe  
10 15 20

cag ttc ctg acc aag tcc acc gct tcc agc gac cgc acc gtg tcc tgg 211  
Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp Arg Thr Val Ser Trp  
25 30 35

gaa gat ggt aac gag tac cca ctg atc gtc gtt gac gtc acc agc gag 259  
Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val Asp Val Thr Ser Glu  
40 45 50

tct cac cca ttc tgg acc ggc gct cag cgt gtc atg gac acc gct ggt 307  
Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val Met Asp Thr Ala Gly  
55 60 65

cgt gtt gag aag ttc gag cgt cgc ttc ggt ggc atg gct cgc cgc aag 355  
Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly Met Ala Arg Arg Lys

70

75

80

85

aag aag gca taggagggaa aacaatggca gtt  
Lys Lys Ala

387

&lt;210&gt; 348

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 348

Met Lys Lys Asp Ile His Pro Asp Tyr His Ala Val Val Phe Gln Asp  
1 5 10 15

Ala Gly Thr Gly Phe Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp  
20 25 30

Arg Thr Val Ser Trp Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val  
35 40 45

Asp Val Thr Ser Glu Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val  
50 55 60

Met Asp Thr Ala Gly Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly  
65 70 75 80

Met Ala Arg Arg Lys Lys Lys Ala  
85

&lt;210&gt; 349

&lt;211&gt; 285

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(262)

&lt;223&gt; RXA02636

&lt;400&gt; 349

tcactctgac cggtttccacc aaggggtctga aggtcattga ccgacgacggc atcgaagccg 60

ttgttgctca gattcgcgca cgtggggaga agatctaaag atg gca cgt aat gat 115  
Met Ala Arg Asn Asp  
1 5

atc cgc cct atc atc aag ctg aag tct act gct ggc act ggt tac acc 163  
Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala Gly Thr Gly Tyr Thr  
10 15 20

tat gtc acc cgt aag aac aag cgc aac aac ccg gac cgt att tcc ctc 211  
Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro Asp Arg Ile Ser Leu  
25 30 35

atg aag tac gat cca gta gtc cgt aag cac gtc gaa ttc cgc gag gag 259  
Met Lys Tyr Asp Pro Val Val Arg Lys His Val Glu Phe Arg Glu Glu  
40 45 50

cga taatcaatgg ctaagaagtc aaa  
Arg

285

<210> 350  
<211> 54  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 350  
Met Ala Arg Asn Asp Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala  
1 5 10 15  
Gly Thr Gly Tyr Thr Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro  
20 25 30  
Asp Arg Ile Ser Leu Met Lys Tyr Asp Pro Val Val Arg Lys His Val  
35 40 45  
Glu Phe Arg Glu Glu Arg  
50

<210> 351  
<211> 264  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(241)  
<223> RXA01423

<400> 351  
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gtccggtgat ccgtcaacaa aatatttagg agtgtttcac atg gca aag ggc aag 115  
Met Ala Lys Gly Lys  
1 5  
cgg acg ttc cag ccg aac aac cgt cgt cgt gca cgt gtt cac ggt ttc 163  
Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala Arg Val His Gly Phe  
10 15 20  
cgt ctt cgt atg cgt acc cgt gca ggt cgt gca att gtt gcg gct cgt 211  
Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala Ile Val Ala Ala Arg  
25 30 35  
cgt cgc aag ggt cgc gca aag ctg acc gcg taatttttta gcgtcaccac 261  
Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala  
40 45  
aat 264

<210> 352  
<211> 47  
<212> PRT  
<213> Corynebacterium glutamicum

&lt;400&gt; 352

Met Ala Lys Gly Lys Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala  
1 5 10 15

Arg Val His Gly Phe Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala  
20 25 30

Ile Val Ala Ala Arg Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala  
35 40 45

&lt;210&gt; 353

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(292)

&lt;223&gt; RXA02419

&lt;400&gt; 353

gaaacccgcg caaagcagga cggacgaaac atgacaatgg ttctcgggtcc ggtgcgcaag 60

ggcaagaaat aatcacgaat aggggtttaag gacaactttc atg aag aac aag acc 115  
Met Lys Asn Lys Thr  
1 5

cac aag ggc acc gca aag cgc gtt aag gtg act ggc tcc ggc aag ctc 163  
His Lys Gly Thr Ala Lys Arg Val Lys Val Thr Gly Ser Gly Lys Leu  
10 15 20

gtt cgc gag cag gca aac cgc cgc cac ctt ctc gag ggc aag tca tct 211  
Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu Glu Gly Lys Ser Ser  
25 30 35

acc cgc act cgt cgc ctg aag ggc atc gtt gag gtt gac aag gcc gac 259  
Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu Val Asp Lys Ala Asp  
40 45 50

acc aag cgc atg aag cgc ctg ctc ggc aag gct taagtttaaa accttcgcct 312  
Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala  
55 60

aaa 315

&lt;210&gt; 354

&lt;211&gt; 64

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 354

Met Lys Asn Lys Thr His Lys Gly Thr Ala Lys Arg Val Lys Val Thr  
1 5 10 15

Gly Ser Gly Lys Leu Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu  
20 25 30

Glu Gly Lys Ser Ser Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu  
35 40 45

Val Asp Lys Ala Asp Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala  
 50 55 60

<210> 355  
 <211> 1581  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1558)  
 <223> RXA02190

<400> 355  
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 ccattatcta atttcctatc catttcggag caattttacat atg ccc acc aac aat 115  
 Met Pro Thr Asn Asn  
 1 5  
 gca cct cag gta gcc atc aac gac att ggc tct gct gag gac ttc ctt 163  
 Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser Ala Glu Asp Phe Leu  
 10 15 20  
 gca gca atc gac gca acc atc aag tac ttc aac gat ggc gat atc gtt 211  
 Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn Asp Gly Asp Ile Val  
 25 30 35  
 gaa ggc acc gtg gta aag gtc gat cgt gac gag gta ctt ctc gac atc 259  
 Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu Val Leu Leu Asp Ile  
 40 45 50  
 gga tac aag acc gag ggt gtc atc cca tcc cgc gag ctg tcc atc aag 307  
 Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg Glu Leu Ser Ile Lys  
 55 60 65  
 cac gat gtc gat cca gac gag gtc gtc gaa gtc ggc gac caa att gac 355  
 His Asp Val Asp Pro Asp Glu Val Val Glu Val Gly Asp Gln Ile Asp  
 70 75 80 85  
 gca ctt gtc ctc acc aag gaa gac aaa gaa ggt cgt ctg atc ctt tcc 403  
 Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly Arg Leu Ile Leu Ser  
 90 95 100  
 aag aag cgt gct cag tac gag cgt gct tgg ggc gcc atc gag gag ctc 451  
 Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly Ala Ile Glu Glu Leu  
 105 110 115  
 aag gaa aag gac gag cca gtt acc ggt acc gtc atc gag gtc gtc aag 499  
 Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val Ile Glu Val Val Lys  
 120 125 130  
 ggt ggc ctc atc atc gac atc ggt ctc cgt ggc ttc ctg cct gca tcc 547  
 Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly Phe Leu Pro Ala Ser  
 135 140 145

ctc gtt gag atg cgt cgc gtc cgc gac ctg gat ccg tac atc ggc cag Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp Pro Tyr Ile Gly Gln 150 155 160 165	595
gag ctc gaa gct aag atc atc gag ctg gac aag aac cgc aac aac gtc Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys Asn Arg Asn Asn Val 170 175 180	643
gtt ctg tcc cgt cgc gca ttc ctc gag cag acc cag tct gag gtc cgc Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr Gln Ser Glu Val Arg 185 190 195	691
tcc gag ttc ctg cac cag ctc cag aag ggc cag gtc cgc aag ggc gtc Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln Val Arg Lys Gly Val 200 205 210	739
gtc tct tcc atc gtc aac ttc ggc gca ttc gtc gat ctc ggc ggt gtc Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val Asp Leu Gly Gly Val 215 220 225	787
gac gga ctg gtt cac gtt tcc gag ctg tcc tgg aag cac atc gac cac Asp Gly Leu Val His Val Ser Glu Leu Ser Trp Lys His Ile Asp His 230 235 240 245	835
cca tct gag gtt gtc acc gtc ggc gac gaa gtc acc gtt gag gtt ctc Pro Ser Glu Val Val Thr Val Gly Asp Glu Val Thr Val Glu Val Leu 250 255 260	883
gag gtc gat ctc gac cgc gag cgc gtc tcc ctg tcc ctg aag gct acc Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu Ser Leu Lys Ala Thr 265 270 275	931
cag gaa gac cca tgg cgc gtc ttc gct cgc act cac gct gtg ggc cag Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr His Ala Val Gly Gln 280 285 290	979
atc gtt cca ggc aag gtc acc aag ctg gtt cca ttc ggt gcg ttc gtt Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro Phe Gly Ala Phe Val 295 300 305	1027
cgc gtc gaa gag ggc atc gaa ggc ctc gtc cac atc tcc gag ctg gct Arg Val Glu Glu Gly Ile Glu Gly Leu Val His Ile Ser Glu Leu Ala 310 315 320 325	1075
cag cgc cac gtc gag gtt ccg gac cag gtt gtc gca gtt ggc gaa gag Gln Arg His Val Glu Val Pro Asp Gln Val Val Ala Val Gly Glu Glu 330 335 340	1123
gtc atg gtc aag gtc atc gac atc gat ctc gag cgt cgt cgt atc tcc Val Met Val Lys Val Ile Asp Ile Asp Leu Glu Arg Arg Arg Ile Ser 345 350 355	1171
ctg tcc ctc aag cag gct gac gag gac tac acc gaa gag ttc gac cca Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr Glu Glu Phe Asp Pro 360 365 370	1219
tcc aag tac gga atg gct gac tcc tac gac gag cag ggt aac tac atc Ser Lys Tyr Gly Met Ala Asp Ser Tyr Asp Glu Gln Gly Asn Tyr Ile 375 380 385	1267
ttc cct gag ggc ttc gac gcc gag acc aac gaa tgg ctc gaa ggc ttc	1315

Phe Pro Glu Gly Phe Asp Ala Glu Thr Asn Glu Trp Leu Glu Gly Phe  
 390 395 400 405  
 gat gag cag cgt cag gct tgg gaa gct cgc tac gcc gag tcc gag cgt 1363  
 Asp Glu Gln Arg Gln Ala Trp Glu Ala Arg Tyr Ala Glu Ser Glu Arg  
 410 415 420  
 cgc ttc acc gct cac acc gct cag atc gag cgt cgt cgt cag cag gct 1411  
 Arg Phe Thr Ala His Thr Ala Gln Ile Glu Arg Arg Arg Gln Gln Ala  
 425 430 435  
 gaa gag gca gct gcc gag gct ccg gcc ggc aac tac tcc act gat tct 1459  
 Glu Glu Ala Ala Ala Glu Ala Pro Ala Gly Asn Tyr Ser Thr Asp Ser  
 440 445 450  
 gca gaa gat gca cct gca gca gaa gca gtt gaa gag tcc gct ggc tcc 1507  
 Ala Glu Asp Ala Pro Ala Glu Ala Val Glu Ser Ala Gly Ser  
 455 460 465  
 ctc gct tcc gat gag cag ctc gct gct ctt cgc gag aag ctc gca ggt 1555  
 Leu Ala Ser Asp Glu Gln Leu Ala Ala Leu Arg Glu Lys Leu Ala Gly  
 470 475 480 485  
 aac taatagttcc tgcacctctt aag 1581  
 Asn

&lt;210&gt; 356

&lt;211&gt; 486

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Met Pro Thr Asn Asn Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser  
 1 5 10 15  
 Ala Glu Asp Phe Leu Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn  
 20 25 30  
 Asp Gly Asp Ile Val Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu  
 35 40 45  
 Val Leu Leu Asp Ile Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg  
 50 55 60  
 Glu Leu Ser Ile Lys His Asp Val Asp Pro Asp Glu Val Val Glu Val  
 65 70 75 80  
 Gly Asp Gln Ile Asp Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly  
 85 90 95  
 Arg Leu Ile Leu Ser Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly  
 100 105 110  
 Ala Ile Glu Glu Leu Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val  
 115 120 125  
 Ile Glu Val Val Lys Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly  
 130 135 140

Phe Leu Pro Ala Ser Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp  
145 150 155 160

Pro Tyr Ile Gly Gln Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys  
165 170 175

Asn Arg Asn Asn Val Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr  
180 185 190

Gln Ser Glu Val Arg Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln  
195 200 205

Val Arg Lys Gly Val Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val  
210 215 220

Asp Leu Gly Gly Val Asp Gly Leu Val His Val Ser Glu Leu Ser Trp  
225 230 235 240

Lys His Ile Asp His Pro Ser Glu Val Val Thr Val Gly Asp Glu Val  
245 250 255

Thr Val Glu Val Leu Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu  
260 265 270

Ser Leu Lys Ala Thr Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr  
275 280 285

His Ala Val Gly Gln Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro  
290 295 300

Phe Gly Ala Phe Val Arg Val Glu Glu Gly Ile Glu Gly Leu Val His  
305 310 315 320

Ile Ser Glu Leu Ala Gln Arg His Val Glu Val Pro Asp Gln Val Val  
325 330 335

Ala Val Gly Glu Glu Val Met Val Lys Val Ile Asp Ile Asp Leu Glu  
340 345 350

Arg Arg Arg Ile Ser Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr  
355 360 365

Glu Glu Phe Asp Pro Ser Lys Tyr Gly Met Ala Asp Ser Tyr Asp Glu  
370 375 380

Gln Gly Asn Tyr Ile Phe Pro Glu Gly Phe Asp Ala Glu Thr Asn Glu  
385 390 395 400

Trp Leu Glu Gly Phe Asp Glu Gln Arg Gln Ala Trp Glu Ala Arg Tyr  
405 410 415

Ala Glu Ser Glu Arg Arg Phe Thr Ala His Thr Ala Gln Ile Glu Arg  
420 425 430

Arg Arg Gln Gln Ala Glu Glu Ala Ala Ala Glu Ala Pro Ala Gly Asn  
435 440 445

Tyr Ser Thr Asp Ser Ala Glu Asp Ala Pro Ala Ala Glu Ala Val Glu  
450 455 460

Glu Ser Ala Gly Ser Leu Ala Ser Asp Glu Gln Leu Ala Ala Leu Arg



465

470

475

480

Glu Lys Leu Ala Gly Asn  
485

&lt;210&gt; 357

&lt;211&gt; 861

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(838)

&lt;223&gt; RXN01912

&lt;400&gt; 357

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gtgtgcactt tgccaccaga cccgccgctg gaaccctaaag atg cgt cgt ttc atc 115  
Met Arg Arg Phe Ile  
1 5

ttc acc gag cgt aac ggc atc tac atc att gac ctt cag cag acc ctg 163  
Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp Leu Gln Gln Thr Leu  
10 15 20

acc tac atc gat cag gct ttc gag ttc gtc aag gaa acc gtt gct cac 211  
Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys Glu Thr Val Ala His  
25 30 35

ggt ggc acc gtt ctt ttc gtt ggt acc aaa aag cag gct cag gaa gct 259  
Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ala  
40 45 50

gtt cag gtt gag gca gac cgc gtt ggt atg cct tac gtg aac cac cgt 307  
Val Gln Val Glu Ala Asp Arg Val Gly Met Pro Tyr Val Asn His Arg  
55 60 65

tgg ctc ggc ggc atg ctg acc aac ttc cag acc gtt tcc aag cgt ctg 355  
Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr Val Ser Lys Arg Leu  
70 75 80 85

aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac 403  
Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala Ala Glu Asn Gly Tyr  
90 95 100

gag ggt cgc acc aag cgc gaa gtt ctc atg ctg acc cgt gag cgc acc 451  
Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu Thr Arg Glu Arg Thr  
105 110 115

aag ctg gag cgc gtc ctc ggt ggt atc gca gag atg acc cgc gtg cct 499  
Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu Met Thr Arg Val Pro  
120 125 130

tcc gca ctg tgg atc att gac acc aac aag gag cac atc gct gtc gct 547  
Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu His Ile Ala Val Ala  
135 140 145

gag gct cac aag ctg aac atc cca gtt gtt gcc atc ctg gac acc aac 595  
Glu Ala His Lys Leu Asn Ile Pro Val Val Ala Ile Leu Asp Thr Asn

150	155	160	165	
tgt gac cca gac gtt gtt gac ttc cca gtt cct ggt aac gac gac gca				643
Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro Gly Asn Asp Asp Ala				
170		175	180	
atc cgc tcc acc gca ctg ctt tcc cgc gtt atc tcc acc gct gtg gaa				691
Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile Ser Thr Ala Val Glu				
185	190	195		
gag ggt aag aag gca cgc gag gag cgt cag ctg gca gct gct aag gat				739
Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu Ala Ala Ala Lys Asp				
200	205	210		
gca gca ggc gac gca aag cct gag gca gag gaa gca cca gca gca gct				787
Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu Ala Pro Ala Ala Ala				
215	220	225		
gag gct gaa gag gca cct gca gct gag gct gaa gag gca cct gca gct				835
Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala				
230	235	240	245	
gag taagctgccc ttaactgcag ttt				861
Glu				

&lt;210&gt; 358

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp	
1 5 10 15	
Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys	
20 25 30	
Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys	
35 40 45	
Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro	
50 55 60	
Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr	
65 70 75 80	
Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala	
85 90 95	
Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu	
100 105 110	
Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu	
115 120 125	
Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu	
130 135 140	
His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala	

[illegible]

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<210> 359
<211> 894
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(871)
<223> FRXA01912
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<400> 359																	
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gtgtgcactt tgccaccaga cccgccgctg gaacccaaag																	
										atg	cgt	cgt	ttc	atc			115
										Met	Arg	Arg	Phe	Ile			
										1				5			
ttc acc gag cgt aac ggc atc tac atc att gac ctt cag cag acc ctg																	163
Phe	Thr	Glu	Arg	Asn	Gly	Ile	Tyr	Ile	Ile	Asp	Leu	Gln	Gln	Thr	Leu		
				10				15						20			
acc tac atc gat cag gct ttc gag ttc gtc aag gaa acc gtt gct cac																	211
Thr	Tyr	Ile	Asp	Gln	Ala	Phe	Glu	Phe	Val	Lys	Glu	Thr	Val	Ala	His		
			25					30					35				
ggt ggc acc gtt ctt ttc gtt ggt acc aaa aag cag gct cag gaa gct																	259
Gly	Gly	Thr	Val	Leu	Phe	Val	Gly	Thr	Lys	Lys	Gln	Ala	Gln	Glu	Ala		
		40					45					50					
ggt cag gtt gag gca gac cgc gtt ggt atg cct tac gtg aac cac cgt																	307
Val	Gln	Val	Glu	Ala	Asp	Arg	Val	Gly	Met	Pro	Tyr	Val	Asn	His	Arg		
	55					60					65						
tgg ctc ggc ggc atg ctg acc aac ttc cag acc gtt tcc aag cgt ctg																	355
Trp	Leu	Gly	Gly	Met	Leu	Thr	Asn	Phe	Gln	Thr	Val	Ser	Lys	Arg	Leu		
70					75					80					85		
aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac																	403
Asn	Arg	Met	Lys	Glu	Leu	Gln	Ala	Met	Asp	Ala	Ala	Glu	Asn	Gly	Tyr		
				90					95					100			

gag ggt cgc acc aag cgc gaa gtt ctc atg ctg acc cgt gag cgc acc 451  
 Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu Thr Arg Glu Arg Thr  
 105 110 115

aag ctg gag cgc gtc ctc ggt ggt atc gca gag atg acc cgc gtg cct 499  
 Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu Met Thr Arg Val Pro  
 120 125 130

tcc gca ctg tgg atc att gac acc aac aag gag cac atc gct gtc gct 547  
 Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu His Ile Ala Val Ala  
 135 140 145

gag gct cac aag ctg aac atc cca gtt gtt gcc atc ctg gac acc aac 595  
 Glu Ala His Lys Leu Asn Ile Pro Val Val Ala Ile Leu Asp Thr Asn  
 150 155 160 165

tgt gac cca gac gtt gtt gac ttc cca gtt cct ggt aac gac gac gca 643  
 Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro Gly Asn Asp Asp Ala  
 170 175 180

atc cgc tcc acc gca ctg ctt tcc cgc gtt atc tcc acc gct gtg gaa 691  
 Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile Ser Thr Ala Val Glu  
 185 190 195

gag ggt aag aag gca cgc gag gag cgt cag ctg gca gct gct aag gat 739  
 Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu Ala Ala Ala Lys Asp  
 200 205 210

gca gca ggc gac gca aag cct gag gca gag gaa gca cca gca gca gct 787  
 Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu Ala Pro Ala Ala Ala  
 215 220 225

gag gct gaa gag gca cct gca gct gag gct gaa gaa cac ctg cag ctg 835  
 Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu Glu His Leu Gln Leu  
 230 235 240 245

agt aag ctg ccc tta act gca gtt tct gca gtt agc tgaccaattt 881  
 Ser Lys Leu Pro Leu Thr Ala Val Ser Ala Val Ser  
 250 255

aaagccccca cga 894

&lt;210&gt; 360

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 360

Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp  
 1 5 10 15

Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys  
 20 25 30

Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys  
 35 40 45

Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro  
 50 55 60

Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr  
 65 70 75 80  
 Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala  
 85 90 95  
 Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu  
 100 105 110  
 Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu  
 115 120 125  
 Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu  
 130 135 140  
 His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala  
 145 150 155 160  
 Ile Leu Asp Thr Asn Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro  
 165 170 175  
 Gly Asn Asp Asp Ala Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile  
 180 185 190  
 Ser Thr Ala Val Glu Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu  
 195 200 205  
 Ala Ala Ala Lys Asp Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu  
 210 215 220  
 Ala Pro Ala Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu  
 225 230 235 240  
 Glu His Leu Gln Leu Ser Lys Leu Pro Leu Thr Ala Val Ser Ala Val  
 245 250 255

Ser

<210> 361  
 <211> 737  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(714)  
 <223> RXA02041

<400> 361  
 cgt ttg ggc atc act tcc gac tgg aag tcc cat tgg tac gcc gac aag 48  
 Arg Leu Gly Ile Thr Ser Asp Trp Lys Ser His Trp Tyr Ala Asp Lys  
 1 5 10 15  
 tct tac gct gac tac gtc gca gaa gac atc aag att cgc gaa ttc ctg 96  
 Ser Tyr Ala Asp Tyr Val Ala Glu Asp Ile Lys Ile Arg Glu Phe Leu  
 20 25 30  
 tcc aag ggc ctc gac cgt gcc ggc atc gcc gac gtc gtc atc gag cgc 144

Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg  
           35                          40                          45  
 acc cgc gac cgc gtt cgc gta gac atc cac acc gct cgc cca ggc atc 192  
 Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile  
           50                          55                          60  
 gtc att ggt cgt cgt ggc gct gag gct gac cgc atc cgc cgt gag ctc 240  
 Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu  
           65                          70                          75                          80  
 gag aag ctc acc ggc aag cag gtt gcc ctc aac atc ctc gag gtc aag 288  
 Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys  
                           85                          90                          95  
 aac gtc gat gct aac gct aag ctg gtg gca cag tcc atc gct gag cag 336  
 Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln  
                           100                          105                          110  
 ctg acc aac cgc gtg gca ttc cgt cgc gca atg cgc aag gct atc cag 384  
 Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln  
                           115                          120                          125  
 tct gca atg cgt cag cca cag gtt aag ggc atc aag gtc gtg tgc tcc 432  
 Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser  
           130                          135                          140  
 ggt cgt ctc ggc ggt gcc gag atg tcc cgc acc gag cgc tac cac gaa 480  
 Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu  
           145                          150                          155                          160  
 ggt cgc gtt cca ctg cac acc ctt cgc gca gaa atc gat tac ggc acc 528  
 Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr  
                           165                          170                          175  
 tac gag gct cac acc act ttc gga cgc atc ggc gtc aag gtg tgg atc 576  
 Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile  
                           180                          185                          190  
 tac aag ggt gac gtc gtt ggt gga cgt cgc gag agc gag atc aat gca 624  
 Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala  
                           195                          200                          205  
 ccc gca gag cgt cgc ggc cgc ggc gac cgc aac gca cgt ccg cgt cgt 672  
 Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg  
           210                          215                          220  
 ggt ggc cag cgt cgt cag cgt gct gag cag aag cag gag ggc 714  
 Gly Gly Gln Arg Arg Gln Arg Ala Glu Gln Lys Gln Glu Gly  
           225                          230                          235  
 taaacatgct tattcctaag cgc 737

&lt;210&gt; 362

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 362

Arg Leu Gly Ile Thr Ser Asp Trp Lys Ser His Trp Tyr Ala Asp Lys

1	5	10	15
Ser Tyr Ala Asp	Tyr Val Ala Glu Asp	Ile Lys Ile Arg	Glu Phe Leu
20	25	30	
Ser Lys Gly Leu	Asp Arg Ala Gly	Ile Ala Asp Val	Val Ile Glu Arg
35	40	45	
Thr Arg Asp Arg	Val Arg Val Asp	Ile His Thr Ala	Arg Pro Gly Ile
50	55	60	
Val Ile Gly Arg	Arg Gly Ala Glu	Ala Asp Arg Ile	Arg Arg Glu Leu
65	70	75	80
Glu Lys Leu Thr	Gly Lys Gln Val	Ala Leu Asn Ile	Leu Glu Val Lys
85	90	95	
Asn Val Asp Ala	Asn Ala Lys Leu	Val Ala Gln Ser	Ile Ala Glu Gln
100	105	110	
Leu Thr Asn Arg	Val Ala Phe Arg	Arg Ala Met Arg	Lys Ala Ile Gln
115	120	125	
Ser Ala Met Arg	Gln Pro Gln Val	Lys Gly Ile Lys	Val Val Cys Ser
130	135	140	
Gly Arg Leu Gly	Gly Ala Glu Met	Ser Arg Thr Glu	Arg Tyr His Glu
145	150	155	160
Gly Arg Val Pro	Leu His Thr Leu	Arg Ala Glu Ile	Asp Tyr Gly Thr
165	170	175	
Tyr Glu Ala His	Thr Thr Phe Gly	Arg Ile Gly Val	Lys Val Trp Ile
180	185	190	
Tyr Lys Gly Asp	Val Val Gly Gly	Arg Arg Glu Ser	Glu Ile Asn Ala
195	200	205	
Pro Ala Glu Arg	Arg Gly Arg Gly	Asp Arg Asn Ala	Arg Pro Arg Arg
210	215	220	
Gly Gly Gln Arg	Arg Gln Arg Ala	Glu Gln Lys Gln	Glu Gly
225	230	235	

&lt;210&gt; 363

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; RXA00672

&lt;400&gt; 363

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agcgctcgctg cggttaatat ggaaggaaag gtaatacaaaa atg gct cgt tat acc 115

Met Ala Arg Tyr Thr

1

5

ggc cca gca acc cgt aaa tcc cgt cgt ctg cgc gtc gac ctt gtt ggt 163  
 Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg Val Asp Leu Val Gly  
 10 15 20

gga gac atg gcg ttt gag cgc cgt cct tac cct cca gga cag gca ggc 211  
 Gly Asp Met Ala Phe Glu Arg Arg Pro Tyr Pro Pro Gly Gln Ala Gly  
 25 30 35

cgt gca cgc atc aag gag tcc gag tac ctg ctg cag ctc cag gag aag 259  
 Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu Gln Leu Gln Glu Lys  
 40 45 50

cag aag gct cgt ttc atc tac ggc gtc atg gaa aag cag ttc cgt cgt 307  
 Gln Lys Ala Arg Phe Ile Tyr Gly Val Met Glu Lys Gln Phe Arg Arg  
 55 60 65

tac tac gcc gag gct aac cgt cgc gca ggc aag acc ggt gag aac ctg 355  
 Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys Thr Gly Glu Asn Leu  
 70 75 80 85

gtc gtc ctg ctc gag tcc cgc ctc gac aac gtc gtg tac cgc gca ggt 403  
 Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val Val Tyr Arg Ala Gly  
 90 95 100

ctg gca aac acc cgt cgc cag gct cgt cag ctt gtt tcc cac ggt cac 451  
 Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu Val Ser His Gly His  
 105 110 115

ttc acc gtg aac ggc aag gca atc gac gtt cca tct ttc cgc gtt tct 499  
 Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro Ser Phe Arg Val Ser  
 120 125 130

cag tac gac atc atc aat gtt cgt gag aag tcc cag aag atg aac tgg 547  
 Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser Gln Lys Met Asn Trp  
 135 140 145

ttc gaa gag gct cag gac aac ctg gcc gac gca gtc gtc cca gct tgg 595  
 Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala Val Val Pro Ala Trp  
 150 155 160 165

ctc cag gtc gtt cct gag aac ctt cgt atc ctc gtg cac cag ctc cca 643  
 Leu Gln Val Val Glu Asn Leu Arg Ile Leu Val His Gln Leu Pro  
 170 175 180

gag cgc gca cag atc gat atc cca ctg caa gag cag ctc atc gtc gag 691  
 Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu Gln Leu Ile Val Glu  
 185 190 195

ttc tac tcg aag tagtttttgc ttaccggct gcc 726  
 Phe Tyr Ser Lys  
 200

&lt;210&gt; 364

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 364

Met Ala Arg Tyr Thr Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg



1	5	10	15
Val Asp Leu	Val Gly Gly Asp Met	Ala Phe Glu Arg Arg	Pro Tyr Pro
	20	25	30
Pro Gly Gln	Ala Gly Arg Ala Arg	Ile Lys Glu Ser Glu	Tyr Leu Leu
	35	40	45
Gln Leu Gln	Glu Lys Gln Lys Ala Arg	Phe Ile Tyr Gly	Val Met Glu
	50	55	60
Lys Gln Phe	Arg Arg Tyr Tyr Ala Glu	Ala Asn Arg Arg	Ala Gly Lys
	65	70	75
Thr Gly Glu	Asn Leu Val Val Leu Leu	Glu Ser Arg Leu	Asp Asn Val
	85	90	95
Val Tyr Arg	Ala Gly Leu Ala Asn Thr	Arg Arg Gln Ala	Arg Gln Leu
	100	105	110
Val Ser His	Gly His Phe Thr Val Asn	Gly Lys Ala Ile	Asp Val Pro
	115	120	125
Ser Phe Arg	Val Ser Gln Tyr Asp	Ile Ile Asn Val	Arg Glu Lys Ser
	130	135	140
Gln Lys Met	Asn Trp Phe Glu Glu Ala	Gln Asp Asn Leu	Ala Asp Ala
	145	150	155
Val Val Pro	Ala Trp Leu Gln Val Val	Pro Glu Asn Leu	Arg Ile Leu
	165	170	175
Val His Gln	Leu Pro Glu Arg Ala Gln	Ile Asp Ile Pro	Leu Gln Glu
	180	185	190
Gln Leu Ile	Val Glu Phe Tyr Ser Lys		
	195	200	

&lt;210&gt; 365

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(733)

&lt;223&gt; RXA00697

&lt;400&gt; 365

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tgatgaccat	ttctaagaac	atcaacggaa	ggattgcgta	atg	ccg	gga	cgt	gaa	115
				Met	Pro	Gly	Arg	Glu	
				1				5	

cgg	cgt	gac	ggc	gga	cgc	tcc	gcc	gac	gac	aac	aag	caa	aac	gat	cgc	163
Arg	Arg	Asp	Gly	Gly	Arg	Ser	Ala	Asp	Asp	Asn	Lys	Gln	Asn	Asp	Arg	
			10					15						20		

aac	gag	cgt	cgt	ggc	gga	ggc	cgc	cgc	gat	gac	cgt	cgc	aat	cag	cag	211
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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<400> 366
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Lys  Gln  Asn  Asp  Arg  Asn  Glu  Arg  Arg  Gly  Gly  Gly  Arg  Arg  Asp  Asp
              20              25              30

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Arg Arg Asn Gln Gln Gln Asp Glu Arg Ser Gln Tyr Ile Glu Arg Val  
           35                          40                          45  
 Val Thr Ile Asn Arg Val Ser Lys Val Val Lys Gly Gly Arg Arg Phe  
           50                          55                          60  
 Ser Phe Thr Ala Leu Val Ile Val Gly Asp Gly Lys Gly Met Val Gly  
           65                          70                          75                          80  
 Val Gly Tyr Gly Lys Ala Lys Glu Val Pro Ala Ala Ile Gln Lys Gly  
                           85                          90                          95  
 Ala Glu Glu Ala Arg Lys Asn Phe Phe Arg Val Pro Met Val Asn Gly  
                           100                          105                          110  
 Thr Ile Thr His Pro Val Gln Gly Glu Lys Ala Ala Gly Ile Val Met  
           115                          120                          125  
 Leu Lys Pro Ala Ala Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Ala  
           130                          135                          140  
 Arg Pro Val Leu Glu Cys Ala Gly Ile Gln Asp Ile Leu Ser Lys Ser  
           145                          150                          155                          160  
 Leu Gly Ser Asp Asn Ala Ile Asn Val Val His Ala Thr Val Asp Gly  
                           165                          170                          175  
 Leu Lys Gln Leu Val Arg Pro Glu Glu Val Ala Ala Arg Arg Gly Lys  
                           180                          185                          190  
 Thr Ile Glu Glu Val Ala Pro Ala Arg Ile Leu Arg Ala Arg Ala Gly  
           195                          200                          205  
 Gln Glu Ala  
           210

&lt;210&gt; 367

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(367)

&lt;223&gt; RXN00545

&lt;400&gt; 367

gctgacgcaa cgaccctcct gctatgccaa cgacggcatg gccgaaaaaa caattactag 60

accataggag gtgatgaggt ccgtgcgtca atacgaactt atg atc att ctc gat 115  
   Met Ile Ile Leu Asp  
   1                          5

cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163  
 Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu  
                           10                          15                          20

gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211  
 Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp

25	30	35	
ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt			259
Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val			
40	45	50	
tac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc			307
Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu			
55	60	65	
gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg			355
Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu			
70	75	80	85
cga ctc gac aag taaagaactt taaggctcta gag			390
Arg Leu Asp Lys			

<210> 368  
 <211> 89  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 368  
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 Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val  
 20 25 30  
 Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys  
 35 40 45  
 Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala  
 50 55 60  
 Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu  
 65 70 75 80  
 Arg Thr Lys Val Leu Arg Leu Asp Lys  
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<210> 369  
 <211> 355  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(355)  
 <223> FRXA00545

<400> 369  
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 accataggag gtgatgaggt ccgtgcgtca atacgaactt atg atc att ctc gat 115  
 Met Ile Ile Leu Asp  
 1 5

cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163  
Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu  
10 15 20

gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211  
Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp  
25 30 35

ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259  
Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val  
40 45 50

tac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307  
Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu  
55 60 65

gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355  
Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu  
70 75 80 85

<210> 370

<211> 85

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Met Ile Ile Leu Asp Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser  
1 5 10 15

Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val  
20 25 30

Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys  
35 40 45

Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala  
50 55 60

Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu  
65 70 75 80

Arg Thr Lys Val Leu  
85

<210> 371

<211> 588

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(565)

<223> RXA01279

<400> 371

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ggctcggttcc cgctacggcg cgaagagggg ataattaaaa atg cgt aaa tca gca 115  
Met Arg Lys Ser Ala

1 5  
 gct cct aag cgt cca gta gtt cag gac cct gta tac aag tcc gag ctc 163  
 Ala Pro Lys Arg Pro Val Val Gln Asp Pro Val Tyr Lys Ser Glu Leu  
 10 15 20  
 gtt acc cag ctc gta aac aag atc ctc atc ggt ggc aag aag tcc acc 211  
 Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly Gly Lys Lys Ser Thr  
 25 30 35  
 gca gag cgc atc gtc tac ggt gca ctc gag atc tgc cgt gag aag acc 259  
 Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile Cys Arg Glu Lys Thr  
 40 45 50  
 ggc acc gat cca gta gga acc ctc gag aag gct ctc ggc aac gtg cgt 307  
 Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala Leu Gly Asn Val Arg  
 55 60 65  
 cca gac ctc gaa gtt cgt tcc cgc cgt gtt ggt ggc gct acc tac cag 355  
 Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly Gly Ala Thr Tyr Gln  
 70 75 80 85  
 gtg cca gtg gat gtt cgc cca gag cgc gca aac acc ctc gca ctg cgt 403  
 Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn Thr Leu Ala Leu Arg  
 90 95 100  
 tgg ttg gta acc ttc acc cgt cag cgt cgt gag aac acc atg atc gag 451  
 Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu Asn Thr Met Ile Glu  
 105 110 115  
 cgt ctt gca aac gaa ctt ctg gat gca gcc aac ggc ctt ggc gct tcc 499  
 Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn Gly Leu Gly Ala Ser  
 120 125 130  
 gtg aag cgt cgc gaa gac acc cac aag atg gca gag gcc aac cgc gcc 547  
 Val Lys Arg Arg Glu Asp Thr His Lys Met Ala Glu Ala Asn Arg Ala  
 135 140 145  
 ttc gct cac tac cgc tgg tagtactgcc aagacatgaa agc 588  
 Phe Ala His Tyr Arg Trp  
 150 155

&lt;210&gt; 372

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 372

Met Arg Lys Ser Ala Ala Pro Lys Arg Pro Val Val Gln Asp Pro Val  
 1 5 10 15  
 Tyr Lys Ser Glu Leu Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly  
 20 25 30  
 Gly Lys Lys Ser Thr Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile  
 35 40 45  
 Cys Arg Glu Lys Thr Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala  
 50 55 60

Leu Gly Asn Val Arg Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly  
 65 70 75 80  
 Gly Ala Thr Tyr Gln Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn  
 85 90 95  
 Thr Leu Ala Leu Arg Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu  
 100 105 110  
 Asn Thr Met Ile Glu Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn  
 115 120 125  
 Gly Leu Gly Ala Ser Val Lys Arg Arg Glu Asp Thr His Lys Met Ala  
 130 135 140  
 Glu Ala Asn Arg Ala Phe Ala His Tyr Arg Trp  
 145 150 155

&lt;210&gt; 373

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(496)

&lt;223&gt; RXA00694

&lt;400&gt; 373

cgactattga gttcgggtgag cgttgagtgg ccagaaaaca cacgggtaac gtccaagggtg 60  
 ggaaggggaac cccaacgaga aaggcatcag gtcgtctctta atg aca atg act gat 115  
 Met Thr Met Thr Asp  
 1 5  
 cca atc gcc gac atg ctg tcg cgc gtg cgc aat gct agc aat gcg cac 163  
 Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn Ala Ser Asn Ala His  
 10 15 20  
 cac gac acc gtg tcc atg cca tcc tcc aag atc aag gca aac atc gcc 211  
 His Asp Thr Val Ser Met Pro Ser Ser Lys Ile Lys Ala Asn Ile Ala  
 25 30 35  
 gag atc ttg aag cag gaa ggc tac atc gct aac tac acc gtt gag gat 259  
 Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn Tyr Thr Val Glu Asp  
 40 45 50  
 gca aag gtc ggc aag acc ctg tcc ctc gag ctg aag tac agc aac acc 307  
 Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu Lys Tyr Ser Asn Thr  
 55 60 65  
 cgt gag cgc tcc atc gct ggt ctg cgc cgc gtt tcc aag cct ggt ctg 355  
 Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val Ser Lys Pro Gly Leu  
 70 75 80 85  
 cgt gta tac gct aag tcc acc aat ctg cca cag gtt ctg ggc ggc ctt 403  
 Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln Val Leu Gly Gly Leu  
 90 95 100  
 ggc gtg gct atc att tcc acg tca cag ggc ctc ctg acc gac cgt cag 451

Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu Leu Thr Asp Arg Gln  
 105 110 115

gct acc gag aag ggc gta ggc gga gaa gtc ctc gcc tac gtc tgg 496  
 Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu Ala Tyr Val Trp  
 120 125 130

taatagggag gattgactaa ata 519

<210> 374

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Met Thr Met Thr Asp Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn  
 1 5 10 15

Ala Ser Asn Ala His His Asp Thr Val Ser Met Pro Ser Ser Lys Ile  
 20 25 30

Lys Ala Asn Ile Ala Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn  
 35 40 45

Tyr Thr Val Glu Asp Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu  
 50 55 60

Lys Tyr Ser Asn Thr Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val  
 65 70 75 80

Ser Lys Pro Gly Leu Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln  
 85 90 95

Val Leu Gly Gly Leu Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu  
 100 105 110

Leu Thr Asp Arg Gln Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu  
 115 120 125

Ala Tyr Val Trp  
 130

<210> 375

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> RXN02038

<400> 375

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agaagcctga ggccctacgag atcaagaagg tggcccagta atg tca gag cct atc 115  
 Met Ser Glu Pro Ile  
 1 5



cag aac gag aac gta gag agc aac gtc gca gac gct gct gac atc gct 163  
 Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp Ala Ala Asp Ile Ala  
                     10                    15                    20

gca gca acc gct gca acc gag gag ttc acc aac acc atc ggc gat gca 211  
 Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn Thr Ile Gly Asp Ala  
                     25                    30                    35

att gct act gct tcc gaa gaa gag acc atc gag gct gca cca gta gta 259  
 Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu Ala Ala Pro Val Val  
                     40                    45                    50

ctc gac ggc cca atc cag acc gtt ggt cgc cgt aag cgc gcc atc gtt 307  
 Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg Lys Arg Ala Ile Val  
                     55                    60                    65

cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc 355  
 Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg  
                     70                    75                    80                    85

acc ctg gaa gag tac ttc cct aac aag ctg cac cag cag ctg atc aag 403  
 Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His Gln Gln Leu Ile Lys  
                     90                    95                    100

gct cct ttg gtc ctt ctg gac cgc ctg aac caa tgc aac atc gag gct 451  
 Ala Pro Leu Val Leu Leu Asp Arg Leu Asn Gln Cys Asn Ile Glu Ala  
                     105                    110                    115

tct ata aag gga cct aaa tagatcggcc aggttatggc aat 492  
 Ser Ile Lys Gly Pro Lys  
                     120

&lt;210&gt; 376

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 376

Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp  
   1                    5                    10                    15

Ala Ala Asp Ile Ala Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn  
                     20                    25                    30

Thr Ile Gly Asp Ala Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu  
                     35                    40                    45

Ala Ala Pro Val Val Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg  
                     50                    55                    60

Lys Arg Ala Ile Val Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe  
                     65                    70                    75                    80

Lys Cys Asn Gly Arg Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His  
                     85                    90                    95

Gln Gln Leu Ile Lys Ala Pro Leu Val Leu Leu Asp Arg Leu Asn Gln  
                     100                    105                    110

Cys Asn Ile Glu Ala Ser Ile Lys Gly Pro Lys

120

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<220>
<221> CDS
<222> (101)..(409)
<223> FRXA02038
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agaagcctga	ggcctacgag	atcaagaagg	tggcccagta	atg	tca	gag	cct	atc								115
				Met	Ser	Glu	Pro	Ile								
				1				5								
cag	aac	gag	aac	gta	gag	agc	aac	gtc	gca	gac	gct	gct	gac	atc	gct	163
Gln	Asn	Glu	Asn	Val	Glu	Ser	Asn	Val	Ala	Asp	Ala	Ala	Asp	Ile	Ala	
				10					15					20		
gca	gca	acc	gct	gca	acc	gag	gag	ttc	acc	aac	acc	atc	ggc	gat	gca	211
Ala	Ala	Thr	Ala	Ala	Thr	Glu	Glu	Phe	Thr	Asn	Thr	Ile	Gly	Asp	Ala	
			25					30					35			
att	gct	act	gct	tcc	gaa	gaa	gag	acc	atc	gag	gct	gca	cca	gta	gta	259
Ile	Ala	Thr	Ala	Ser	Glu	Glu	Glu	Thr	Ile	Glu	Ala	Ala	Pro	Val	Val	
		40					45					50				
ctc	gac	ggc	cca	atc	cag	acc	gtt	ggt	cgc	cgt	aag	cgc	gcc	atc	gtt	307
Leu	Asp	Gly	Pro	Ile	Gln	Thr	Val	Gly	Arg	Arg	Lys	Arg	Ala	Ile	Val	
	55					60					65					
cgc	gtc	cgc	ctt	gta	gct	ggc	tcc	ggc	gag	ttc	aag	tgc	aac	ggt	cgc	355
Arg	Val	Arg	Leu	Val	Ala	Gly	Ser	Gly	Glu	Phe	Lys	Cys	Asn	Gly	Arg	
70					75				80					85		
acc	ctg	gaa	gag	tac	ttc	cct	aac	aag	ctg	cac	cag	cag	ctg	atc	aag	403
Thr	Leu	Glu	Glu	Tyr	Phe	Pro	Asn	Lys	Leu	His	Gln	Gln	Leu	Ile	Lys	
				90					95					100		
gct	cct														409	
Ala	Pro															

<400> 378  
Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp  
1 5 10 15  
Ala Ala Asp Ile Ala Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn  
20 25 30

Thr Ile Gly Asp Ala Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu  
 35 40 45  
 Ala Ala Pro Val Val Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg  
 50 55 60  
 Lys Arg Ala Ile Val Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe  
 65 70 75 80  
 Lys Cys Asn Gly Arg Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His  
 85 90 95  
 Gln Gln Leu Ile Lys Ala Pro  
 100

<210> 379  
 <211> 426  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(403)  
 <223> RXA01287

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 Val Ala Gly Gln Lys  
 1 5  
 atc cgc att agg ctc aag gcc tac gac cac gaa gcg att gat gcg tct 163  
 Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu Ala Ile Asp Ala Ser  
 10 15 20  
 gca cgc aag atc gtt gag acg gtc acc cgt acg ggt gcc cga gtc gtt 211  
 Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr Gly Ala Arg Val Val  
 25 30 35  
 gga ccg gtg cct ttg cct acc gaa aag aac gta tac gcc gtt att cgt 259  
 Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val Tyr Ala Val Ile Arg  
 40 45 50  
 tct cca cat aag tac aag gac tct cgc gag cac ttc gag atg cgc act 307  
 Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His Phe Glu Met Arg Thr  
 55 60 65  
 cac aag cgc ctg atc gac atc ctc gac ccg acg ccg aag act gtt gat 355  
 His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr Pro Lys Thr Val Asp  
 70 75 80 85  
 gcc ctt atg cgc atc gac ctt ccg gcc agc gtc gac gtg aac att cag 403  
 Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val Asp Val Asn Ile Gln  
 90 95 100  
 tgatcgacgg aatttttggc agc 426

<210> 380

<211> 101  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 380  
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                   20                  25                  30  
 Gly Ala Arg Val Val Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val  
                   35                  40                  45  
 Tyr Ala Val Ile Arg Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His  
                   50                  55                  60  
 Phe Glu Met Arg Thr His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr  
   65                  70                  75                  80  
 Pro Lys Thr Val Asp Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val  
                   85                  90                  95  
 Asp Val Asn Ile Gln  
                   100

<210> 381  
 <211> 113  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(90)  
 <223> RXA00673

<400> 381  
 ctt cag gct gca ggc ctg gag atc ggt tca atc tcc gac gtg acc cca 48  
 Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp Val Thr Pro  
   1                  5                  10                  15  
 cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc gtt 90  
 Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val  
                   20                  25                  30  
 taatagggaa ggaaaggtaa tac 113

<210> 382  
 <211> 30  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 382  
 Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp Val Thr Pro  
   1                  5                  10                  15  
 Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val  
                   20                  25                  30

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<400> 384
Met  Pro  Thr  Ile  Gln  Gln  Leu  Val  Arg  Lys  Ala  Arg  His  Asp  Lys  Ser
   1              5              10              15
Asp  Lys  Val  Ala  Thr  Ala  Ala  Leu  Lys  Gly  Ser  Pro  Gln  Arg  Arg  Gly

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20	25	30
Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala		
35	40	45
Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser		
50	55	60
Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val		
65	70	75
Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys		
85	90	95
Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln		
100	105	110
Ala Arg Ser Arg Tyr Gly Ala Lys Arg Gly		
115	120	

<210> 385  
 <211> 426  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(403)  
 <223> RXA02637

<400> 385  
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 agtccgtaag cacgtcgaat tccgcgagga gcgataatca atg gct aag aag tca 115  
 Met Ala Lys Lys Ser  
 1 5  
 aag atc gcc aag aac gag aag cgc aag gaa atc gtc gcc cgc tac gcg 163  
 Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile Val Ala Arg Tyr Ala  
 10 15 20  
 gag cgt cgc gct gag ctg aag gca att atc agt aac cca aac acc tct 211  
 Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser Asn Pro Asn Thr Ser  
 25 30 35  
 gac gag gat cgt ctg gat gca cag ttc gaa ctg aac agc cag cca cgt 259  
 Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu Asn Ser Gln Pro Arg  
 40 45 50  
 gat gct gct gct gtc cgc gtt cgt aac cgc gac tca cac gat ggt cgc 307  
 Asp Ala Ala Ala Val Arg Val Arg Asn Arg Asp Ser His Asp Gly Arg  
 55 60 65  
 cca cgc ggc tac ctg cgt aag ttc ggt ctt tcc cgt gtc cgt atg cgc 355  
 Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser Arg Val Arg Met Arg  
 70 75 80 85  
 gag atg gct cac cgt ggt gag ctg ccg ggc gtt cgt aag tcc agc tgg 403  
 Glu Met Ala His Arg Gly Glu Leu Pro Gly Val Arg Lys Ser Ser Trp  
 90 95 100

taagggagtt tttaccaatg aag

426

<210> 386

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

Met Ala Lys Lys Ser Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile  
1 5 10 15

Val Ala Arg Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser  
20 25 30

Asn Pro Asn Thr Ser Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu  
35 40 45

Asn Ser Gln Pro Arg Asp Ala Ala Ala Val Arg Val Arg Asn Arg Asp  
50 55 60

Ser His Asp Gly Arg Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser  
65 70 75 80

Arg Val Arg Met Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Val  
85 90 95

Arg Lys Ser Ser Trp  
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<210> 387

<211> 390

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(367)

<223> RXA01487

<400> 387

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Met Ala Leu Thr Ser  
1 5

gag cag aag aag tcc atc ctt tcc gag ttc ggc ctc cac gag acc gac 163  
Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly Leu His Glu Thr Asp  
10 15 20

acc ggt tcc cca gaa gca cag atc gcg ctt ctg acc aac cgc atc aac 211  
Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu Thr Asn Arg Ile Asn  
25 30 35

aac ctc acc gag cac ctc aag ttc cac aag cac gat cac cac tcc cgt 259  
Asn Leu Thr Glu His Leu Lys Phe His Lys His Asp His His Ser Arg  
40 45 50

cgt ggt ctg ctg ctg ctc gtt ggt cgt cgt cgt ggt ctg ctg aag tac 307  
 Arg Gly Leu Leu Leu Leu Val Gly Arg Arg Arg Gly Leu Leu Lys Tyr  
 55 60 65  
 ctg gct gac aac aac gtt gat cgc tac cgt gat ctg atc gca cgc ctc 355  
 Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp Leu Ile Ala Arg Leu  
 70 75 80 85  
 ggc ctg cgt cga taagcctggt ttttccagtc ttt 390  
 Gly Leu Arg Arg

<210> 388  
 <211> 89  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 388  
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 Leu His Glu Thr Asp Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu  
 20 25 30  
 Thr Asn Arg Ile Asn Asn Leu Thr Glu His Leu Lys Phe His Lys His  
 35 40 45  
 Asp His His Ser Arg Arg Gly Leu Leu Leu Leu Val Gly Arg Arg Arg  
 50 55 60  
 Gly Leu Leu Lys Tyr Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp  
 65 70 75 80  
 Leu Ile Ala Arg Leu Gly Leu Arg Arg  
 85

<210> 389  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02752

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 Met Ala Val Lys Ile  
 1 5  
 aag ctc cag cgc ctc ggc aag atc cgt acc ccg cac tac cgc gtt gtc 163  
 Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro His Tyr Arg Val Val  
 10 15 20  
 atc gct gat gca cgc acc aag cgc gac ggc aag gtt atc gag aac atc 211  
 Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys Val Ile Glu Asn Ile



25	30	35	
ggt atc tac gag cca aag gct gag cct tcc gta atc aag atc aac tcc			259
Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val Ile Lys Ile Asn Ser			
40	45	50	
gag cgt gcg cag cac tgg ctc tcc gtt ggc gct cag cca acc gag gct			307
Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala Gln Pro Thr Glu Ala			
55	60	65	
gtt gca gcg ctg ctc aag gtg acc ggc gac tgg cag aag ttc aag ggc			355
Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp Gln Lys Phe Lys Gly			
70	75	80	85
atc gag ggc gca gaa ggc acc ctc cgt gtt gca gag cct aag cca tcc			403
Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala Glu Pro Lys Pro Ser			
90	95	100	
aag ctt gag ctg ttc aac cag gct ctt tct gag gct aac aac ggc cca			451
Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu Ala Asn Asn Gly Pro			
105	110	115	
acc gct gaa gcc atc act gaa aag aag aag aag gct cgc gag gac aag			499
Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys Ala Arg Glu Asp Lys			
120	125	130	
gaa gct aag gaa gca gct gag aag gct gct gct gaa aag gct gcc gct			547
Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala			
135	140	145	
gca gag tcc gaa gag gct cca gct gag gaa gct gct gca gaa gag gca			595
Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala Ala Ala Glu Glu Ala			
150	155	160	165
taagccactt ttgtttgtac ttc			618

&lt;210&gt; 390

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 390

Met Ala Val Lys Ile Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro
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His Tyr Arg Val Val Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys
20 25 30

Val Ile Glu Asn Ile Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val
35 40 45

Ile Lys Ile Asn Ser Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala
50 55 60

Gln Pro Thr Glu Ala Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp
65 70 75 80

Gln Lys Phe Lys Gly Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala
85 90 95

Glu Pro Lys Pro Ser Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu  
 100 105 110

Ala Asn Asn Gly Pro Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys  
 115 120 125

Ala Arg Glu Asp Lys Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala  
 130 135 140

Glu Lys Ala Ala Ala Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala  
 145 150 155 160

Ala Ala Glu Glu Ala  
 165

<210> 391  
 <211> 384  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02389

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tgtacacaac tttaactaga aagttcaaga ggtatttgcg atg gca aac atc aag 115  
 Met Ala Asn Ile Lys  
 1 5

tct cag atc aag cgt aac aag acc aac gag aag gct cgt ctg cgt aac 163  
 Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys Ala Arg Leu Arg Asn  
 10 15 20

cag gca gtt cgc tcc gca gtc cgc acc gag atc cgc aag ttc aac gct 211  
 Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile Arg Lys Phe Asn Ala  
 25 30 35

gcg att gaa gca ggc gac aag gat gca gct cag gct cag ctc cgt acc 259  
 Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln Ala Gln Leu Arg Thr  
 40 45 50

gct tcc cgc gca ctg gac aag gca gta acc aag ggt gtc ttc cac atc 307  
 Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys Gly Val Phe His Ile  
 55 60 65

aac aac gct gct aac aag aag tcc aac atg gct acc gct ttc aac aag 355  
 Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala Thr Ala Phe Asn Lys  
 70 75 80 85

ctt ggc taatttttgg ctcttttgaa aat 384  
 Leu Gly

<210> 392  
 <211> 87  
 <212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Ala Asn Ile Lys Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys  
 1 5 10 15  
 Ala Arg Leu Arg Asn Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile  
 20 25 30  
 Arg Lys Phe Asn Ala Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln  
 35 40 45  
 Ala Gln Leu Arg Thr Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys  
 50 55 60  
 Gly Val Phe His Ile Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala  
 65 70 75 80  
 Thr Ala Phe Asn Lys Leu Gly  
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<210> 393

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXA00671

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 Met Leu Ile Ser Gln  
 1 5  
 cgc cca acc atc acc gag gaa ttt gtt aat aac gca cgt tcc cgg ttt 163  
 Arg Pro Thr Ile Thr Glu Glu Phe Val Asn Asn Ala Arg Ser Arg Phe  
 10 15 20  
 gtc atc gag cca ctg gag cca ggt ttt ggc tac acc ctc ggt aac tcc 211  
 Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr Thr Leu Gly Asn Ser  
 25 30 35  
 ctg cgc cgt acc ctg ctg tcc tcc att cct gga gca gca gta acc agc 259  
 Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly Ala Ala Val Thr Ser  
 40 45 50  
 gtc aag att gac ggt gta ctc cac gag ttc acc acc atc agc ggt gtt 307  
 Val Lys Ile Asp Gly Val Leu His Glu Phe Thr Thr Ile Ser Gly Val  
 55 60 65  
 aag gaa gat gtc tct gac atc atc ttg aac atc aag gga ttg gtt ttg 355  
 Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile Lys Gly Leu Val Leu  
 70 75 80 85  
 tct tct gat tcc gat gag cca gtt gtt atg cag ctg gtc aag gaa ggc 403  
 Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln Leu Val Lys Glu Gly

90										95					100					
cca	gga	gtt	gta	act	gca	ggt	gac	att	cag	cca	cca	gca	ggc	gtg	gag	451				
Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Gly	Val	Glu					
105										110					115					
atc	cac	aac	ccg	gat	ctg	cac	att	gca	acc	ctg	aac	gag	acc	gcc	aag	499				
Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu	Asn	Glu	Thr	Ala	Lys					
120										125					130					
att	gag	atc	gag	ctc	atc	gtc	gag	cgt	gga	cgt	ggc	tac	gtt	ccc	gca	547				
Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala					
135										140					145					
act	gtt	act	gca	acc	ggt	gga	gag	atc	ggc	cgc	att	ccg	gtc	gat	cag	595				
Thr	Val	Thr	Ala	Thr	Gly	Gly	Glu	Ile	Gly	Arg	Ile	Pro	Val	Asp	Gln					
150										155					160					
atc	tac	tcc	cca	gta	ctg	aag	gtc	agc	tac	aag	gtt	gaa	gct	act	cgt	643				
Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Ser	Tyr	Lys	Val	Glu	Ala	Thr	Arg					
170										175					180					
gtt	gag	cag	cgc	acc	gac	ttt	gac	aag	ctg	gtc	atc	gac	gtt	gag	acc	691				
Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu	Val	Ile	Asp	Val	Glu	Thr					
185										190					195					
aag	aac	tct	att	acc	gca	cgt	gac	gcc	ctg	gcg	tcg	gca	ggt	aag	acc	739				
Lys	Asn	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Leu	Ala	Ser	Ala	Gly	Lys	Thr					
200										205					210					
ctg	gtt	gag	ctg	ttc	ggc	ctc	gca	cgc	gag	ctg	aac	atc	gca	gcc	gag	787				
Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu	Leu	Asn	Ile	Ala	Ala	Glu					
215										220					225					
ggc	atc	gag	atc	gga	cca	tct	cct	cag	gag	acc	gag	tac	atc	gct	gcc	835				
Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Gln	Glu	Thr	Glu	Tyr	Ile	Ala	Ala					
230										235					240					
tac	agc	atg	cca	atc	gag	gat	ctg	gac	ttc	tct	gtc	cgt	tcc	tac	aac	883				
Tyr	Ser	Met	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Ser	Val	Arg	Ser	Tyr	Asn					
250										255					260					
tgc	ctc	aag	cgc	gaa	gac	atc	cac	acc	gtg	ggt	gaa	ctc	gca	gag	cgc	931				
Cys	Leu	Lys	Arg	Glu	Asp	Ile	His	Thr	Val	Gly	Glu	Leu	Ala	Glu	Arg					
265										270					275					
gct	gag	tcc	gat	ttg	ctg	gat	atc	cgc	aac	ttc	gga	cag	aag	tcg	atc	979				
Ala	Glu	Ser	Asp	Leu	Leu	Asp	Ile	Arg	Asn	Phe	Gly	Gln	Lys	Ser	Ile					
280										285					290					
aac	gag	gta	aag	atc	aag	ctt	gct	ggc	ctg	ggt	ctg	acc	ctg	aag	gat	1027				
Asn	Glu	Val	Lys	Ile	Lys	Leu	Ala	Gly	Leu	Gly	Leu	Thr	Leu	Lys	Asp					
295										300					305					
gct	cct	gaa	gac	ttc	gat	cct	tca	act	ctt	gaa	ggt	tat	gac	gcc	gaa	1075				
Ala	Pro	Glu	Asp	Phe	Asp	Pro	Ser	Thr	Leu	Glu	Gly	Tyr	Asp	Ala	Glu					
310										315					320					
act	ggt	ggc	tac	atc	gat	gtc	gag	gcg	gaa	gat	tcc	gag	taagtcgcat			1124				
Thr	Gly	Gly	Tyr	Ile	Asp	Val	Glu	Ala	Glu	Asp	Ser	Glu								
330										335										

ggtccaattc atg

1137

&lt;210&gt; 394

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 394

Met Leu Ile Ser Gln Arg Pro Thr Ile Thr Glu Glu Phe Val Asn Asn  
1 5 10 15

Ala Arg Ser Arg Phe Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr  
20 25 30

Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly  
35 40 45

Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr  
50 55 60

Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile  
65 70 75 80

Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln  
85 90 95

Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro  
100 105 110

Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu  
115 120 125

Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg  
130 135 140

Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg  
145 150 155 160

Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys  
165 170 175

Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val  
180 185 190

Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala  
195 200 205

Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu  
210 215 220

Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr  
225 230 235 240

Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser  
245 250 255

Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly  
260 265 270

<400> 395																
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Met Ala Arg Leu Ala																5
1																
ggt gtt gac ctc cca cgc aac aag cgt atg gaa gtc gct ctc acc tac																163
Gly Val Asp Leu Pro Arg Asn Lys Arg Met Glu Val Ala Leu Thr Tyr																20
10 15																
atc tac gga atc ggc cca gcc cgt tcc aag cag ctt ctc gag gag acc																211
Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln Leu Leu Glu Glu Thr																35
25 30																
gga atc tcc cca gac ctg cgc acc gac aac ctc act gat gag cag atc																259
Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu Thr Asp Glu Gln Ile																50
40 45																
gct gct ctt cgt gac gtt att gaa ggc acc tgg aag gtc gag ggt gac																307
Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp Lys Val Glu Gly Asp																65
55 60																
ctc cgc cgc cag gta caa gct gac atc cgt cgc aag atc gaa atc ggc																355
Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg Lys Ile Glu Ile Gly																85
70 75 80																
tgc tac cag ggt att cgc cac cgc cgt ggc ctg cct gtt cgt ggt cag																403
Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu Pro Val Arg Gly Gln																100
90 95																
cgc acc aag acc aat gcg cgt act cgt aag ggt cct aag aag acg atc																451
Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro Lys Lys Thr Ile																115
105 110																

gcc gga aag aag aag taaaaatgcc tcctaaagca cgc  
 Ala Gly Lys Lys Lys  
 120

489

<210> 396  
 <211> 122  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 396  
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 Val Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln  
 20 25 30  
 Leu Leu Glu Glu Thr Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu  
 35 40 45  
 Thr Asp Glu Gln Ile Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp  
 50 55 60  
 Lys Val Glu Gly Asp Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg  
 65 70 75 80  
 Lys Ile Glu Ile Gly Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu  
 85 90 95  
 Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly  
 100 105 110  
 Pro Lys Lys Thr Ile Ala Gly Lys Lys Lys  
 115 120

<210> 397  
 <211> 372  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(349)  
 <223> RXN03139

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 Met Lys Gln Arg Asn  
 1 5  
 aac gct aag cgc gtc cgc ctt gag cag act cgc cgc cca aag aag aac 163  
 Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg Arg Pro Lys Lys Asn  
 10 15 20  
 ccg ctg aag gca gcg ggc atc gag aag gtg gac tac aag gac atc aac 211  
 Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp Tyr Lys Asp Ile Asn  
 25 30 35

acc ctt cgt cag ttc atc tcc gac cgc cac aag atc cgt tca cgt cgt 259  
Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys Ile Arg Ser Arg Arg  
40 45 50

gtc acc ggt ctg acc ccg cag cag cag cgc gag gtt gca acc gcc gtg 307  
Val Thr Gly Leu Thr Pro Gln Gln Gln Arg Glu Val Ala Thr Ala Val  
55 60 65

aag aac gca cgc gaa atg gct ctc ctg ccg ttc acc agc cgc 349  
Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe Thr Ser Arg  
70 75 80

taagactggg aataacgtaa cag 372

<210> 398  
<211> 83  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 398  
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Arg Pro Lys Lys Asn Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp  
20 25 30

Tyr Lys Asp Ile Asn Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys  
35 40 45

Ile Arg Ser Arg Arg Val Thr Gly Leu Thr Pro Gln Gln Gln Arg Glu  
50 55 60

Val Ala Thr Ala Val Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe  
65 70 75 80

Thr Ser Arg

<210> 399  
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<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(502)  
<223> RXN00673

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agggtcctaa gaagacgatc gccggaaaga agaagtaaaa atg cct cct aaa gca 115  
Met Pro Pro Lys Ala  
1 5

cgc act aac gcg cgc cgc aca ggc cgt cgc gtt gta aaa aag aac gtt 163  
Arg Thr Asn Ala Arg Arg Thr Gly Arg Arg Val Val Lys Lys Asn Val  
10 15 20



gct aac ggc aac gct tac atc aag tcc acc ttt aac aac acc atc gtt 211  
Ala Asn Gly Asn Ala Tyr Ile Lys Ser Thr Phe Asn Asn Thr Ile Val  
25 30 35

tcg atc act gat acc aac ggt gct gta atc tct tgg gct tcc tct ggg 259  
Ser Ile Thr Asp Thr Asn Gly Ala Val Ile Ser Trp Ala Ser Ser Gly  
40 45 50

cac gtc gga ttc aag ggc tca cgt aag tcc act ccg ttc gct gct cag 307  
His Val Gly Phe Lys Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln  
55 60 65

atg gct gca gag aac gct gcc cgc aag gca atg gat cac ggc atg aag 355  
Met Ala Ala Glu Asn Ala Ala Arg Lys Ala Met Asp His Gly Met Lys  
70 75 80 85

aag gtt gac gtt ttc gtc aag ggc cca gga tca ggc cgc gag act gca 403  
Lys Val Asp Val Phe Val Lys Gly Pro Gly Ser Gly Arg Glu Thr Ala  
90 95 100

atc cgt tcc ctt cag gct gca ggc ctg gag atc ggt tca atc tcc gac 451  
Ile Arg Ser Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp  
105 110 115

gtg acc cca cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc 499  
Val Thr Pro Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg  
120 125 130

gtt taatagggaa ggaaaggtaa tac 525  
Val

&lt;210&gt; 400

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 400

Met Pro Pro Lys Ala Arg Thr Asn Ala Arg Arg Thr Gly Arg Arg Val  
1 5 10 15

Val Lys Lys Asn Val Ala Asn Gly Asn Ala Tyr Ile Lys Ser Thr Phe  
20 25 30

Asn Asn Thr Ile Val Ser Ile Thr Asp Thr Asn Gly Ala Val Ile Ser  
35 40 45

Trp Ala Ser Ser Gly His Val Gly Phe Lys Gly Ser Arg Lys Ser Thr  
50 55 60

Pro Phe Ala Ala Gln Met Ala Ala Glu Asn Ala Ala Arg Lys Ala Met  
65 70 75 80

Asp His Gly Met Lys Lys Val Asp Val Phe Val Lys Gly Pro Gly Ser  
85 90 95

Gly Arg Glu Thr Ala Ile Arg Ser Leu Gln Ala Ala Gly Leu Glu Ile  
100 105 110

Gly Ser Ile Ser Asp Val Thr Pro Gln Pro His Asn Gly Cys Arg Pro

115

120

125

Pro Lys Arg Arg Arg Val  
130

&lt;210&gt; 401

&lt;211&gt; 684

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(661)

&lt;223&gt; RXN00714

&lt;400&gt; 401

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accatcacat ataagacatc tcatgatcta acattttcttc atg gct acg att aca 115  
Met Ala Thr Ile Thr  
1 5

cgc acc gac aga ctg atc ctc gta ccg ctc act gtt gag ctc gaa gac 163  
Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr Val Glu Leu Glu Asp  
10 15 20

gag gcc cac cag att tac tct gat tct cga atc tgg gaa cac cgc ccc 211  
Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile Trp Glu His Arg Pro  
25 30 35

cag gcg cgt cac acc aac gtg cgt gtc acg cgc gac atc atc aag cgc 259  
Gln Ala Arg His Thr Asn Val Arg Val Thr Arg Asp Ile Ile Lys Arg  
40 45 50

acc aat gaa agc tgg ggc aag aaa gac ctt ggc ccc tgg ggt gtt tac 307  
Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly Pro Trp Gly Val Tyr  
55 60 65

ctc cgt gac cgc cca tcg gaa ttc gtt ggc gtt ggt ggc gtt gaa ctc 355  
Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu  
70 75 80 85

atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta 403  
Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu  
90 95 100

tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc 451  
Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala  
105 110 115

acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc 499  
Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr  
120 125 130

aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc 547  
Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro  
135 140 145

gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct 595  
Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro

150						155						160						165	
gat	gtg	aga	att	tat	tct	gac	cgt	ccg	cta	tcg	gat	gaa	att	ctt	gaa	643			
Asp	Val	Arg	Ile	Tyr	Ser	Asp	Arg	Pro	Leu	Ser	Asp	Glu	Ile	Leu	Glu				
				170					175					180					

atg ctc aag caa cga cca tagaccagaa aatctcaccc ctt 684  
Met Leu Lys Gln Arg Pro  
185

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<210> 402
<211> 187
<212> PRT
<213> Corynebacterium glutamicum
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<400> 402  
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Val Glu Leu Glu Asp Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile  
20 25 30

Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg  
35 40 45

Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly  
50 55 60

Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val  
65 70 75 80

Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg  
85 90 95

Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn  
100 105 110

Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr  
115 120 125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys  
130 135 140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp  
145 150 155 160

Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser  
165 170 175

Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro  
180 185

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<210> 403
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS

&lt;222&gt; (101)..(1105)

&lt;223&gt; RXN00897

&lt;400&gt; 403

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ttgacctgga tgccgggtga agatgaggat cctttcgggc atg acg cct agt ctt 115
                                   Met Thr Pro Ser Leu
                                   1           5

ccc cgt ttc cgc agc cag aaa cct gcc gtc ggc gat cgt gtt gtt gca 163
Pro Arg Phe Arg Ser Gln Lys Pro Ala Val Gly Asp Arg Val Val Ala
                        10                      15                20

cgt cgc cgg att cct ggt gcc aat gtg cat tgg aca gat gtc att ggc 211
Arg Arg Arg Ile Pro Gly Ala Asn Val His Trp Thr Asp Val Ile Gly
                        25                      30                35

cat gtg att ggg gtg gat ccg ttg gtg gtt cgc ccg cag tcg gtt ggt 259
His Val Ile Gly Val Asp Pro Leu Val Val Arg Pro Gln Ser Val Gly
                        40                      45                50

ggg atg ccg tct gat gcg gaa gaa att gtc att cct gat gat cag ctt 307
Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile Pro Asp Asp Gln Leu
                        55                      60                65

gag gtg att aag att ttg tcg ccg cgc acc att agg aat tcg gat att 355
Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile Arg Asn Ser Asp Ile
                        70                      75                80                85

cgt gcg gtg gag gtt gcc acg gcg aag gcc ttt ccg ggg ctg gtc aat 403
Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe Pro Gly Leu Val Asn
                        90                      95                100

gag tgg cat gat ggt tgg ctg ctg cgt gcc ggt gat ggc att gcg gag 451
Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly Asp Gly Ile Ala Glu
                        105                      110                115

cgt tct aat tct gcg tcg cca ctc ggc cca agt gtc ggt tct gag ccg 499
Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser Val Gly Ser Glu Pro
                        120                      125                130

gta ccg atg gag gat att tcg cgg ttt tat gca cgt cac gat ctc ccc 547
Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala Arg His Asp Leu Pro
                        135                      140                145

gtg aag ctg cac att ccg gag cgg att ggt cgg cct gcg cag aaa gtc 595
Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg Pro Ala Gln Lys Val
                        150                      155                160                165

att gac gcc gat ccc cag aaa tgg gtg atg ggc ccg gag att ttg gtg 643
Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly Pro Glu Ile Leu Val
                        170                      175                180

atg acg aaa tct ttg gac cat gtg gag tcg cac gaa ttg ccc ggt ggc 691
Met Thr Lys Ser Leu Asp His Val Glu Ser His Glu Leu Pro Gly Gly
                        185                      190                195

cta gaa ttt agc gtc gat aag cag cct gac cag gag tgg ctg ggc atg 739
Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln Glu Trp Leu Gly Met
                        200                      205                210

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tac cat ttc cgc gga cag gcg ttg ccc gct cac gcc ctt gag ctt ttg 787  
 Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His Ala Leu Glu Leu Leu  
 215 220 225  
 cgc acg caa atc gag ggc cgc atg ggg ttc ggg cgc ctg acc acg ccg 835  
 Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly Arg Leu Thr Thr Pro  
 230 235 240 245  
 gcg ggg caa acc gtc gcg atc acg cgc gcc acc atc acg gct gcg gag 883  
 Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr Ile Thr Ala Ala Glu  
 250 255 260  
 gag cgc ata ttt ttg ggc tat tca gcg gtc gag gtg gat cct gct ttt 931  
 Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu Val Asp Pro Ala Phe  
 265 270 275  
 cga cgt cag ggg ctg ggc acc gcg ctc ggc tcg cgc atc cag gag tgg 979  
 Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser Arg Ile Gln Glu Trp  
 280 285 290  
 ggc gcc gag caa cac gca cag gag gca tat ctc cag gtt gtc gcc cat 1027  
 Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu Gln Val Val Ala His  
 295 300 305  
 aat gaa gca ggt atc ggc ctg tat caa aag ctc ggg ttc agt gaa cac 1075  
 Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu Gly Phe Ser Glu His  
 310 315 320 325  
 cac cga cac cgg tac gcc gaa cgg aaa ttc taaaatccaa aacagctagg 1125  
 His Arg His Arg Tyr Ala Glu Arg Lys Phe  
 330 335

gta 1128

<210> 404  
 <211> 335  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 404  
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 Asp Arg Val Val Ala Arg Arg Arg Ile Pro Gly Ala Asn Val His Trp  
 20 25 30  
 Thr Asp Val Ile Gly His Val Ile Gly Val Asp Pro Leu Val Val Arg  
 35 40 45  
 Pro Gln Ser Val Gly Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile  
 50 55 60  
 Pro Asp Asp Gln Leu Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile  
 65 70 75 80  
 Arg Asn Ser Asp Ile Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe  
 85 90 95  
 Pro Gly Leu Val Asn Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly

100	105	110
Asp Gly Ile Ala Glu Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser 115 120 125		
Val Gly Ser Glu Pro Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala 130 135 140		
Arg His Asp Leu Pro Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg 145 150 155 160		
Pro Ala Gln Lys Val Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly 165 170 175		
Pro Glu Ile Leu Val Met Thr Lys Ser Leu Asp His Val Glu Ser His 180 185 190		
Glu Leu Pro Gly Gly Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln 195 200 205		
Glu Trp Leu Gly Met Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His 210 215 220		
Ala Leu Glu Leu Leu Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly 225 230 235 240		
Arg Leu Thr Thr Pro Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr 245 250 255		
Ile Thr Ala Ala Glu Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu 260 265 270		
Val Asp Pro Ala Phe Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser 275 280 285		
Arg Ile Gln Glu Trp Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu 290 295 300		
Gln Val Val Ala His Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu 305 310 315 320		
Gly Phe Ser Glu His His Arg His Arg Tyr Ala Glu Arg Lys Phe 325 330 335		

&lt;210&gt; 405

&lt;211&gt; 2322

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2299)

&lt;223&gt; RXN01380

&lt;400&gt; 405

acacattccg ggtagaattg cccaaatgtc atcaatttct cgaacgattg ctctcgaact 60

cggcgtcaaaa gatgaacaag tcgaggccgc catcaagctc ttg gat gaa gga aac 115

Leu Asp Glu Gly Asn

1

5

acc gtt ccg ttc atc gcc agg tac cgc aag gaa atc act ggg gga ctc	163
Thr Val Pro Phe Ile Ala Arg Tyr Arg Lys Glu Ile Thr Gly Gly Leu	
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gat gat acc caa ctg cgt gac ctg gaa gaa cgc ctc agt tac ctc cgt	211
Asp Asp Thr Gln Leu Arg Asp Leu Glu Glu Arg Leu Ser Tyr Leu Arg	
25 30 35	
gag ctg gag gat cgt aaa caa agc atc ctc gcc gcg att gag gaa caa	259
Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala Ala Ile Glu Glu Gln	
40 45 50	
ggc aaa ctc acc gac gat tta cgc tcg ctg att ttg gga tgc gac acc	307
Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile Leu Gly Cys Asp Thr	
55 60 65	
aag gct cgc ctg gag gat ctg tac ctg ccg ttc aaa aaa cgg cgc aag	355
Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe Lys Lys Arg Arg Lys	
70 75 80 85	
acg aag gcc gat atc gct agg gag gcg ggc ctg gag ggg ctc gtc gat	403
Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu Glu Gly Leu Val Asp	
90 95 100	
aag ctt atc gac gcc ccg tcc ctc gac gcc gca gcg cag gca gct gca	451
Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala Ala Gln Ala Ala Ala	
105 110 115	
ttt acg act gag ggc ttt gag gat tcc aaa aaa gtt ttg gat ggc gct	499
Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys Val Leu Asp Gly Ala	
120 125 130	
cgc gcc att ttg att gac cgc ttc gcg ctc gat gcc gat ttg gtg ggc	547
Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp Ala Asp Leu Val Gly	
135 140 145	
gag gtg cgt gag caa atg tat cgc gcg ggt tcc atg gcg gca tcg gtg	595
Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser Met Ala Ala Ser Val	
150 155 160 165	
gtg gcg ggc aag gag cag gaa ggc gca aag ttc aag gac tac ttt gag	643
Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe Lys Asp Tyr Phe Glu	
170 175 180	
ttt tcc gaa cct ttt gac aag ctt cca tct cac cga att ttg gcg ctg	691
Phe Ser Glu Pro Phe Asp Lys Leu Pro Ser His Arg Ile Leu Ala Leu	
185 190 195	
ctg cgc ggt gaa aac gaa ggt gtg ctg agc ctc aac ctc gat gcg ggc	739
Leu Arg Gly Glu Asn Glu Gly Val Leu Ser Leu Asn Leu Asp Ala Gly	
200 205 210	
gac gac ata atc tac gaa ggt ttg atc gcc gac cga ttc tcc ctg gac	787
Asp Asp Ile Ile Tyr Glu Gly Leu Ile Ala Asp Arg Phe Ser Leu Asp	
215 220 225	
acc cac act tct agc tgg ctg gct gag gct gtg cgc tgg ggt tgg cgc	835
Thr His Thr Ser Ser Trp Leu Ala Glu Ala Val Arg Trp Gly Trp Arg	
230 235 240 245	

acc aaa ctg tat gtg tcc tcc gga ttg gat gtg cgc atg cgt ctg aaa	883
Thr Lys Leu Tyr Val Ser Ser Gly Leu Asp Val Arg Met Arg Leu Lys	
250 255 260	
gaa aaa gca gag gaa ggc gca ctc gat gtg ttt gcc acc aac ctc cgc	931
Glu Lys Ala Glu Glu Gly Ala Leu Asp Val Phe Ala Thr Asn Leu Arg	
265 270 275	
gac gtt ctc ctt gca gct ccc gct ggt cag cgc tcc aca att ggc ctt	979
Asp Val Leu Leu Ala Ala Pro Ala Gly Gln Arg Ser Thr Ile Gly Leu	
280 285 290	
gac ccg gga ttc cgc aac ggt gtg aaa gta gct gtc gtg gat tcc acc	1027
Asp Pro Gly Phe Arg Asn Gly Val Lys Val Ala Val Val Asp Ser Thr	
295 300 305	
ggt aag gat gtt gcc acc acg atc gtc tac cca cac cag ccc caa aac	1075
Gly Lys Asp Val Ala Thr Ile Val Tyr Pro His Gln Pro Gln Asn	
310 315 320 325	
cgc tgg aag gaa gcc gta tcc gaa ctg gct aac ctg tgc gcg acc cac	1123
Arg Trp Lys Glu Ala Val Ser Glu Leu Ala Asn Leu Cys Ala Thr His	
330 335 340	
ggt gtg gaa ctc atg gcg atc ggc aac gga acc gcc tcg agg gaa acg	1171
Gly Val Glu Leu Met Ala Ile Gly Asn Gly Thr Ala Ser Arg Glu Thr	
345 350 355	
gaa aaa ctc gcc ggc gaa gta gct gac atg atc aaa gcc gca ggt ggc	1219
Glu Lys Leu Ala Gly Glu Val Ala Asp Met Ile Lys Ala Ala Gly Gly	
360 365 370	
acg cga cca acc ccc gtg gtg gtc tcc gaa tcg ggc gca tcc gtg tac	1267
Thr Arg Pro Thr Pro Val Val Val Ser Glu Ser Gly Ala Ser Val Tyr	
375 380 385	
tcg gca tca ccg atc gca gcc gaa gaa ttc ccc gac atg gac gtc tcc	1315
Ser Ala Ser Pro Ile Ala Ala Glu Glu Phe Pro Asp Met Asp Val Ser	
390 395 400 405	
ctc cgc ggt gca gtt tct atc gcg agg cga ctc cag gat cca ctg gcg	1363
Leu Arg Gly Ala Val Ser Ile Ala Arg Arg Leu Gln Asp Pro Leu Ala	
410 415 420	
gag ctc gtc aag att gag ccc aaa gcc atc gga gtc ggc cag tac caa	1411
Glu Leu Val Lys Ile Glu Pro Lys Ala Ile Gly Val Gly Gln Tyr Gln	
425 430 435	
cac gat gtc aac cag gtt gca ctt gcc aaa acc ctt gat ggt gtc gtc	1459
His Asp Val Asn Gln Val Ala Leu Ala Lys Thr Leu Asp Gly Val Val	
440 445 450	
gaa gac gca gta aac gca gtc gga gtt aac ctc aac acc gca tcc gca	1507
Glu Asp Ala Val Asn Ala Val Gly Val Asn Leu Asn Thr Ala Ser Ala	
455 460 465	
cca ctt ctt acc cga gtt gcc gga gtg acc tcc acc ttg gca aac aat	1555
Pro Leu Leu Thr Arg Val Ala Gly Val Thr Ser Thr Leu Ala Asn Asn	
470 475 480 485	
atc gtg gcc tac cgc aac gaa aac ggt gga ttc tcc tcc cga aaa gaa	1603



Ile Val Ala Tyr Arg Asn Glu Asn Gly Gly Phe Ser Ser Arg Lys Glu	
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ctg aac aaa gtt cct cgc ctg gga ccc aaa gcc ttt gaa cag tgt gct	1651
Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala Phe Glu Gln Cys Ala	
505 510 515	
ggc ttc ctc cgc att tct gga tcc acc gac cct ctc gac gcc tcc gct	1699
Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro Leu Asp Ala Ser Ala	
520 525 530	
gtt cac ccc gag gcg tac cca gtt gtt cgc aac att gcg aaa gcc aca	1747
Val His Pro Glu Ala Tyr Pro Val Val Arg Asn Ile Ala Lys Ala Thr	
535 540 545	
gga ttg gat gtc tcg gga ctg atc gga aac tct gcg gtg ctc acc aaa	1795
Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser Ala Val Leu Thr Lys	
550 555 560 565	
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Leu Lys Pro Ala Asp Phe Ala Asp Glu Arg Phe Gly Ile Pro Thr Val	
570 575 580	
acc gac atc atc gcc gag ctg gat aaa ccc gga cgt gac ccc cgc cca	1891
Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly Arg Asp Pro Arg Pro	
585 590 595	
gaa ttc aaa acc gcc agc ttc aaa gaa ggc gtg gag aaa atc tcc gac	1939
Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val Glu Lys Ile Ser Asp	
600 605 610	
ctc aca ccc ggc atg atc ctg gaa gga act gtc acc aac gtt gcg gcg	1987
Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val Thr Asn Val Ala Ala	
615 620 625	
ttc ggc gca ttc gtt gac gtg gga gtg cac cga gat ggc ctc gtt cac	2035
Phe Gly Ala Phe Val Asp Val Gly Val His Arg Asp Gly Leu Val His	
630 635 640 645	
gtt tcc gcg atg agc gac aaa ttc atc tcc aac ccc cac gaa gtt gtt	2083
Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn Pro His Glu Val Val	
650 655 660	
cgc tct ggt gag gtc gtg aag gta aag gtc atg gaa gtt gac gtc gac	2131
Arg Ser Gly Glu Val Val Lys Val Lys Val Met Glu Val Asp Val Asp	
665 670 675	
cgc aaa cgc atc ggc ctt tcc ctc cgc ttg acc gat gaa ccc ggt gcc	2179
Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr Asp Glu Pro Gly Ala	
680 685 690	
cca gct ccg caa aag cgc gga aac cga cca gcc aaa cag cag cga gct	2227
Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala Lys Gln Gln Arg Ala	
695 700 705	
ccg caa aaa cag tcc gct aag ccc gcc aca ggt tcc atg gca gat gct	2275
Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly Ser Met Ala Asp Ala	
710 715 720 725	
tta cga cgc gcc ggc ctc ggt ggc taaggcaact ttcaaacc aa gcg	2322
Leu Arg Arg Ala Gly Leu Gly Gly	

730

&lt;210&gt; 406

&lt;211&gt; 733

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Leu Asp Glu Gly Asn Thr Val Pro Phe Ile Ala Arg Tyr Arg Lys Glu  
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Ile Thr Gly Gly Leu Asp Asp Thr Gln Leu Arg Asp Leu Glu Glu Arg  
20 25 30

Leu Ser Tyr Leu Arg Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala  
35 40 45

Ala Ile Glu Glu Gln Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile  
50 55 60

Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe  
65 70 75 80

Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu  
85 90 95

Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala  
100 105 110

Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys  
115 120 125

Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp  
130 135 140

Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser  
145 150 155 160

Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe  
165 170 175

Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu Pro Ser His  
180 185 190

Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val Leu Ser Leu  
195 200 205

Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu Ile Ala Asp  
210 215 220

Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala Glu Ala Val  
225 230 235 240

Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly Leu Asp Val  
245 250 255

Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu Asp Val Phe  
260 265 270

Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala Gly Gln Arg

275					280					285						
Ser	Thr	Ile	Gly	Leu	Asp	Pro	Gly	Phe	Arg	Asn	Gly	Val	Lys	Val	Ala	
290					295					300						
Val	Val	Asp	Ser	Thr	Gly	Lys	Asp	Val	Ala	Thr	Thr	Ile	Val	Tyr	Pro	
305					310					315					320	
His	Gln	Pro	Gln	Asn	Arg	Trp	Lys	Glu	Ala	Val	Ser	Glu	Leu	Ala	Asn	
325					330					335						
Leu	Cys	Ala	Thr	His	Gly	Val	Glu	Leu	Met	Ala	Ile	Gly	Asn	Gly	Thr	
340					345					350						
Ala	Ser	Arg	Glu	Thr	Glu	Lys	Leu	Ala	Gly	Glu	Val	Ala	Asp	Met	Ile	
355					360					365						
Lys	Ala	Ala	Gly	Gly	Thr	Arg	Pro	Thr	Pro	Val	Val	Val	Ser	Glu	Ser	
370					375					380						
Gly	Ala	Ser	Val	Tyr	Ser	Ala	Ser	Pro	Ile	Ala	Ala	Glu	Glu	Phe	Pro	
385					390					395					400	
Asp	Met	Asp	Val	Ser	Leu	Arg	Gly	Ala	Val	Ser	Ile	Ala	Arg	Arg	Leu	
405					410					415						
Gln	Asp	Pro	Leu	Ala	Glu	Leu	Val	Lys	Ile	Glu	Pro	Lys	Ala	Ile	Gly	
420					425					430						
Val	Gly	Gln	Tyr	Gln	His	Asp	Val	Asn	Gln	Val	Ala	Leu	Ala	Lys	Thr	
435					440					445						
Leu	Asp	Gly	Val	Val	Glu	Asp	Ala	Val	Asn	Ala	Val	Gly	Val	Asn	Leu	
450					455					460						
Asn	Thr	Ala	Ser	Ala	Pro	Leu	Leu	Thr	Arg	Val	Ala	Gly	Val	Thr	Ser	
465					470					475					480	
Thr	Leu	Ala	Asn	Asn	Ile	Val	Ala	Tyr	Arg	Asn	Glu	Asn	Gly	Gly	Phe	
485					490					495						
Ser	Ser	Arg	Lys	Glu	Leu	Asn	Lys	Val	Pro	Arg	Leu	Gly	Pro	Lys	Ala	
500					505					510						
Phe	Glu	Gln	Cys	Ala	Gly	Phe	Leu	Arg	Ile	Ser	Gly	Ser	Thr	Asp	Pro	
515					520					525						
Leu	Asp	Ala	Ser	Ala	Val	His	Pro	Glu	Ala	Tyr	Pro	Val	Val	Arg	Asn	
530					535					540						
Ile	Ala	Lys	Ala	Thr	Gly	Leu	Asp	Val	Ser	Gly	Leu	Ile	Gly	Asn	Ser	
545					550					555					560	
Ala	Val	Leu	Thr	Lys	Leu	Lys	Pro	Ala	Asp	Phe	Ala	Asp	Glu	Arg	Phe	
565					570					575						
Gly	Ile	Pro	Thr	Val	Thr	Asp	Ile	Ile	Ala	Glu	Leu	Asp	Lys	Pro	Gly	
580					585					590						
Arg	Asp	Pro	Arg	Pro	Glu	Phe	Lys	Thr	Ala	Ser	Phe	Lys	Glu	Gly	Val	
595					600					605						

Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val  
 610 615 620  
 Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly Val His Arg  
 625 630 635 640  
 Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn  
 645 650 655  
 Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val Lys Val Met  
 660 665 670  
 Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr  
 675 680 685  
 Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala  
 690 695 700  
 Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly  
 705 710 715 720  
 Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly  
 725 730

<210> 407  
 <211> 1286  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1263)  
 <223> RXA00157

<400> 407  
 gcc cgc atc gtt gct gag cag cgt gag gcg gaa gcc gtc gaa aag aaa 48  
 Ala Arg Ile Val Ala Glu Gln Arg Glu Ala Glu Ala Val Glu Lys Lys  
 1 5 10 15  
 gtc cag acc gag gct gca att gcc gca aac agc gag cag ctc aat gtc 96  
 Val Gln Thr Glu Ala Ala Ile Ala Asn Ser Glu Gln Leu Asn Val  
 20 25 30  
 ttg act acc aat cgc agt acc ttg gtt gcc cag cgt gat ggg gct gag 144  
 Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu  
 35 40 45  
 cgc aac ttg gcc atc gct cgt gcg cag gcg gat aat ctg caa ggt cag 192  
 Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln  
 50 55 60  
 cgt gct gag tac gag gaa ttc cag cag gca gag cag gct cgc atc cag 240  
 Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln  
 65 70 75 80  
 gcg gaa gcg gaa gct cag gct gct gcg gag gag aag cgt cgt gcc gat 288  
 Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp  
 85 90 95

gag gct gct gca cag gca gcc gct gaa gct caa gaa gct gcc cag caa	336
Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln	
100 105 110	
gct cag gcg gcg gag gaa gcc caa gcc gcg caa gca gct gag aca gca	384
Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala	
115 120 125	
caa gcc caa gcc gcg caa gct gcg gaa acc caa gct gca caa gcc gcg	432
Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala	
130 135 140	
caa gct cag gca gaa gcg aat gat cgt gcc gcc gcg caa cag cgt gct	480
Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala	
145 150 155 160	
gca gag gct caa gca gca gcg gaa cag gcg caa cgt gag gct gac gct	528
Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala	
165 170 175	
cag gcg gcc aac gat gcc caa gct cag gca ctg cgt gaa cag gcg ctc	576
Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu	
180 185 190	
acc gca gcc tcc atc gct gcg gct gct cta att gcg gcg agc cag tcc	624
Thr Ala Ala Ser Ile Ala Ala Ala Leu Ile Ala Ala Ser Gln Ser	
195 200 205	
agc cat gcc act act caa aat cct tac cca act gat gaa gac gcg gat	672
Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp	
210 215 220	
ccg acc gat att gcg gac atc caa ggc cca acg cag cca ggt acg ggt	720
Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly	
225 230 235 240	
gag tct gga gat tcc cag agc aac tcc agc gac aac gat tcc aca ggc	768
Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly	
245 250 255	
aac gat tcc aca ggc tct gac tct tca gat tca gat tcc tcc ggc aac	816
Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn	
260 265 270	
gat tct tca gag gtt att tcc ggc gat cgt tcc gct cag att gag act	864
Asp Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr	
275 280 285	
gtg att gcg cgc gcc atg agc cag ttg ggt gtg cag tac gca tgg ggt	912
Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly	
290 295 300	
ggc ggt aac gct aat ggc cca act ctg ggt atc cgt gac ggt ggc gtg	960
Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val	
305 310 315 320	
gcg gac tct tac ggc gat tac aac aag gtt ggc ttc gac tgc tct gga	1008
Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly	
325 330 335	
ctg acc ttg tat gcg ttt gcg ggt gtg gga att tca ctt cct cac tac	1056

Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr  
 340 345 350  
 acg ggc tac cag tac cag cac ggc acc aag gtg tcg cct tct gag atg 1104  
 Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met  
 355 360 365  
 caa cgt ggc gat ctg atc ttc tat ggt ccg gga gcg tct cag cac gtg 1152  
 Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val  
 370 375 380  
 gca att tac ctc ggt gat ggt cag atg att gag gct ccg aat tcg ggt 1200  
 Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly  
 385 390 395 400  
 tct gtc gtg aag att tct cct gtt cgc tgg agc gga atg acc gag agc 1248  
 Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser  
 405 410 415  
 gtg gta cgc ctc att tagtttctc ctatgaatct tga 1286  
 Val Val Arg Leu Ile  
 420  
 <210> 408  
 <211> 421  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 408  
 Ala Arg Ile Val Ala Glu Gln Arg Glu Ala Glu Ala Val Glu Lys Lys  
 1 5 10 15  
 Val Gln Thr Glu Ala Ala Ile Ala Ala Asn Ser Glu Gln Leu Asn Val  
 20 25 30  
 Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu  
 35 40 45  
 Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln  
 50 55 60  
 Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln  
 65 70 75 80  
 Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp  
 85 90 95  
 Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln  
 100 105 110  
 Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala  
 115 120 125  
 Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala  
 130 135 140  
 Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala  
 145 150 155 160  
 Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala

165					170					175					
Gln	Ala	Ala	Asn	Asp	Ala	Gln	Ala	Gln	Ala	Leu	Arg	Glu	Gln	Ala	Leu
			180					185					190		
Thr	Ala	Ala	Ser	Ile	Ala	Ala	Ala	Ala	Leu	Ile	Ala	Ala	Ser	Gln	Ser
			195				200					205			
Ser	His	Ala	Thr	Thr	Gln	Asn	Pro	Tyr	Pro	Thr	Asp	Glu	Asp	Ala	Asp
	210					215					220				
Pro	Thr	Asp	Ile	Ala	Asp	Ile	Gln	Gly	Pro	Thr	Gln	Pro	Gly	Thr	Gly
225					230					235					240
Glu	Ser	Gly	Asp	Ser	Gln	Ser	Asn	Ser	Ser	Asp	Asn	Asp	Ser	Thr	Gly
				245					250					255	
Asn	Asp	Ser	Thr	Gly	Ser	Asp	Ser	Ser	Asp	Ser	Asp	Ser	Ser	Gly	Asn
			260					265						270	
Asp	Ser	Ser	Glu	Val	Ile	Ser	Gly	Asp	Arg	Ser	Ala	Gln	Ile	Glu	Thr
			275				280					285			
Val	Ile	Ala	Arg	Ala	Met	Ser	Gln	Leu	Gly	Val	Gln	Tyr	Ala	Trp	Gly
	290					295					300				
Gly	Gly	Asn	Ala	Asn	Gly	Pro	Thr	Leu	Gly	Ile	Arg	Asp	Gly	Gly	Val
305					310					315					320
Ala	Asp	Ser	Tyr	Gly	Asp	Tyr	Asn	Lys	Val	Gly	Phe	Asp	Cys	Ser	Gly
				325					330					335	
Leu	Thr	Leu	Tyr	Ala	Phe	Ala	Gly	Val	Gly	Ile	Ser	Leu	Pro	His	Tyr
			340					345					350		
Thr	Gly	Tyr	Gln	Tyr	Gln	His	Gly	Thr	Lys	Val	Ser	Pro	Ser	Glu	Met
		355					360						365		
Gln	Arg	Gly	Asp	Leu	Ile	Phe	Tyr	Gly	Pro	Gly	Ala	Ser	Gln	His	Val
	370					375					380				
Ala	Ile	Tyr	Leu	Gly	Asp	Gly	Gln	Met	Ile	Glu	Ala	Pro	Asn	Ser	Gly
385					390					395					400
Ser	Val	Val	Lys	Ile	Ser	Pro	Val	Arg	Trp	Ser	Gly	Met	Thr	Glu	Ser
			405						410					415	
Val	Val	Arg	Leu	Ile											
			420												

&lt;210&gt; 409

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(949)

&lt;223&gt; RXA00208

cggccaattt tttctttttgt ggggggtgcct cttacgcatt tccctgaattt ttgttaggct															60
tgcctaggtc agttaaagat atatcgataa gaggttttcc atg aac act cca gcg															115
Met Asn Thr Pro Ala															5
1															
ccc cgc aaa cga cgc gaa atg aaa atc aag aca gca acc gtc act ggt	163														
Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr Ala Thr Val Thr Gly															
10 15 20															
gtg cgt caa att tcc ccc gat ctc atc cgc ttc agc ttc gac tgc cca	211														
Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe Ser Phe Asp Cys Pro															
25 30 35															
gaa atc gtt ggc gcc gac ctg ggg ttc acg gac cat tac atc aag atc	259														
Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp His Tyr Ile Lys Ile															
40 45 50															
ctc ttc gtg cca gca ggt gcg gat tac tcc tgg cct ttc gac atg gca	307														
Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp Pro Phe Asp Met Ala															
55 60 65															
gaa att gcg gaa acc cag ccc cgt gag ctg caa cca gtg cgc cgc acc	355														
Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln Pro Val Arg Arg Thr															
70 75 80 85															
tac act ttc cgc acg gtt gac act gtc gca ggc aca ttt gac ata gat	403														
Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly Thr Phe Asp Ile Asp															
90 95 100															
ttc gtt gcg cac ggc acc gat ggc ctt gcc ggt cct tgg gcg cag cag	451														
Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly Pro Trp Ala Gln Gln															
105 110 115															
gca cag gta ggt gat gtc atc gcg ttc ggc ggc cca ggt ggc gca tgg	499														
Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly Pro Gly Ala Trp															
120 125 130															
aag cca gaa acc acc tat gag cac tac gtt ctc gca ggc gat gaa gcc	547														
Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu Ala Gly Asp Glu Ala															
135 140 145															
gca gca ccc gca att ttc gca gcc tta gaa cac cta ccc gcc ggc acc	595														
Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His Leu Pro Ala Gly Thr															
150 155 160 165															
acc gcc aaa gcc ttc att gaa atc tcc tcc aac gaa gcg cgt ttc aac	643														
Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn Glu Ala Arg Phe Asn															
170 175 180															
gcc cca gcc agc gac aac atc gag gtt gtc tgg gtg ccc cgc gac ggc	691														
Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp Val Pro Arg Asp Gly															
185 190 195															
gcc acc cac ggt aca ttg ctt atc gac gcc ctc cgc cag gac ggc tac	739														
Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu Arg Gln Asp Gly Tyr															
200 205 210															
cca acc aag aaa act tcc tgg ttc atc cac gga gtc gcc gaa atg gtg	787														
Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly Val Ala Glu Met Val															



215	220	225	
aag gaa acc cgc aaa ttc ctc ttc gtg gaa ggc aac gta gac aaa gct			835
Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly Asn Val Asp Lys Ala			
230	235	240	245
gat gca tcc att tcc gga tac tgg cgc ctt ggc atg acc gaa gac cag			883
Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly Met Thr Glu Asp Gln			
250	255		260
tgg cag gcc tcc aag cgg gag ttc aat gag caa aat gag gca gaa gaa			931
Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln Asn Glu Ala Glu Glu			
265	270		275
ctc gcg ctc agc aag gca taagggcaag gggttctaga aag			972
Leu Ala Leu Ser Lys Ala			
280			

&lt;210&gt; 410

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 410

Met Asn Thr Pro Ala Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr
1 5 10 15

Ala Thr Val Thr Gly Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe
20 25 30

Ser Phe Asp Cys Pro Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp
35 40 45

His Tyr Ile Lys Ile Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp
50 55 60

Pro Phe Asp Met Ala Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln
65 70 75 80

Pro Val Arg Arg Thr Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly
85 90 95

Thr Phe Asp Ile Asp Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly
100 105 110

Pro Trp Ala Gln Gln Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly
115 120 125

Pro Gly Gly Ala Trp Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu
130 135 140

Ala Gly Asp Glu Ala Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His
145 150 155 160

Leu Pro Ala Gly Thr Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn
165 170 175

Glu Ala Arg Phe Asn Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp
180 185 190

Val Pro Arg Asp Gly Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu  
 195 200 205

Arg Gln Asp Gly Tyr Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly  
 210 215 220

Val Ala Glu Met Val Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly  
 225 230 235 240

Asn Val Asp Lys Ala Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly  
 245 250 255

Met Thr Glu Asp Gln Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln  
 260 265 270

Asn Glu Ala Glu Glu Leu Ala Leu Ser Lys Ala  
 275 280

&lt;210&gt; 411

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26)..(388)

&lt;223&gt; RXA00967

&lt;400&gt; 411

caactagaaa atgactgggg gcgat atg ccg gtg cag gac gca ggc gaa cgc 52  
 Met Pro Val Gln Asp Ala Gly Glu Arg  
 1 5

aac aac aat gac cgg cca gtg atg ccg gga gag atc ctc cgt gag gaa 100  
 Asn Asn Asn Asp Arg Pro Val Met Pro Gly Glu Ile Leu Arg Glu Glu  
 10 15 20 25

ttc atg gag cct ttg ggg ctg tcc caa aac ggc ttg gcg cgg gca ata 148  
 Phe Met Glu Pro Leu Gly Leu Ser Gln Asn Gly Leu Ala Arg Ala Ile  
 30 35 40

gga gtg cca cca cgc agg att aat gag atc gtg cac ggc aaa cgc gca 196  
 Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ala  
 45 50 55

atc acg gca gac act gcg ctg cgt tta gct gct tat tta ggt ccc gat 244  
 Ile Thr Ala Asp Thr Ala Leu Arg Leu Ala Ala Tyr Leu Gly Pro Asp  
 60 65 70

cca cag ttt tgg ctc aac ttg cag acc cac tac gac ctg tcg gtg acg 292  
 Pro Gln Phe Trp Leu Asn Leu Gln Thr His Tyr Asp Leu Ser Val Thr  
 75 80 85

tat tta gat gcg cgc aca ctg ttg gaa gcg atc aag cct tat gat cgt 340  
 Tyr Leu Asp Ala Arg Thr Leu Leu Glu Ala Ile Lys Pro Tyr Asp Arg  
 90 95 100 105

cag caa aat gtg gct cgg acc ctg aat ccg ctt cag gag agc tcg cag 388  
 Gln Gln Asn Val Ala Arg Thr Leu Asn Pro Leu Gln Glu Ser Ser Gln  
 110 115 120

taggagtcgc ctctggtcgg ggc

411

&lt;210&gt; 412

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Met Pro Val Gln Asp Ala Gly Glu Arg Asn Asn Asn Asp Arg Pro Val  
 1 5 10 15

Met Pro Gly Glu Ile Leu Arg Glu Glu Phe Met Glu Pro Leu Gly Leu  
 20 25 30

Ser Gln Asn Gly Leu Ala Arg Ala Ile Gly Val Pro Pro Arg Arg Ile  
 35 40 45

Asn Glu Ile Val His Gly Lys Arg Ala Ile Thr Ala Asp Thr Ala Leu  
 50 55 60

Arg Leu Ala Ala Tyr Leu Gly Pro Asp Pro Gln Phe Trp Leu Asn Leu  
 65 70 75 80

Gln Thr His Tyr Asp Leu Ser Val Thr Tyr Leu Asp Ala Arg Thr Leu  
 85 90 95

Leu Glu Ala Ile Lys Pro Tyr Asp Arg Gln Gln Asn Val Ala Arg Thr  
 100 105 110

Leu Asn Pro Leu Gln Glu Ser Ser Gln  
 115 120

&lt;210&gt; 413

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(358)

&lt;223&gt; RXA01149

&lt;400&gt; 413

atttttaaca agaacctttt tcaaacattc tttttataag ttttttccat attggttgat 60

ccccaccat cgggatccct gatccacgaa aggagtgttc gtg gta gct ccg cag 115  
 Val Val Ala Pro Gln  
 1 5

tcc cgg aaa ccg cag cac cct ggt gag att ttg agt gaa cgt ttc ctc 163  
 Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu Ser Glu Arg Phe Leu  
 10 15 20

gaa ccc cga gga atc agc cac tac gat ctc gcc aaa acc ctc cac atc 211  
 Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala Lys Thr Leu His Ile  
 25 30 35

acc gaa gca acc atc gcc aat ttc gtt gaa ggt cgc acc gac ctc acc 259  
 Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly Arg Thr Asp Leu Thr  
           40                          45                          50

atc gga ctt gca gta cgc ctc tcc cgc tca ttc gat ttg agc aca cag 307  
 Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe Asp Leu Ser Thr Gln  
           55                          60                          65

gaa tgg atc gca ctg cag cgc acc ttt gat cag gct cat cgt cga tct 355  
 Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln Ala His Arg Arg Ser  
           70                          75                          80                          85

gct taaaagtttt tagcttcac gaa 381  
 Ala

<210> 414  
 <211> 86  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 414  
 Val Val Ala Pro Gln Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu  
   1                          5                          10                          15

Ser Glu Arg Phe Leu Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala  
           20                          25                          30

Lys Thr Leu His Ile Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly  
           35                          40                          45

Arg Thr Asp Leu Thr Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe  
           50                          55                          60

Asp Leu Ser Thr Gln Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln  
           65                          70                          75                          80

Ala His Arg Arg Ser Ala  
                           85

<210> 415  
 <211> 1989  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1966)  
 <223> RXA01305

<400> 415  
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tcaacaggca ctgtgggacc ccttcacttt gaaagacatc atg cgc ccc tct tcc 115  
   Met Arg Pro Ser Ser  
   1                          5

cgg cca ctt ggc ctc gtc cta tgc acc gca ctg gca tca acg atc atc 163  
 Arg Pro Leu Gly Leu Val Leu Cys Thr Ala Leu Ala Ser Thr Ile Ile

10										15					20					
acc gtt ccc gca gcg tcc gcc cag gag cca gcg ctt ctc gat gcc tcc	211																			
Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala Leu Leu Asp Ala Ser																				
25 30 35																				
gcc atc gcc cca cat acc gcc agc tac ggc tac tac gtt gat gca tgg	259																			
Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr Tyr Val Asp Ala Trp																				
40 45 50																				
gac acc aac gtt tcc act gat ctg aat cca tca agt aat gca gct gtt	307																			
Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser Ser Asn Ala Ala Val																				
55 60 65																				
ggc gta ctg gag gaa atg ctt gag ctg tgg acc cca ggc gaa gaa tgg	355																			
Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr Pro Gly Glu Glu Trp																				
70 75 80 85																				
aac acc ggc gtc aag gtt gac ccc acc gtg ctg gat tcc aac atc gca	403																			
Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu Asp Ser Asn Ile Ala																				
90 95 100																				
cag tct gtg gca atc tcc cag cag gcg acc gat gct cag caa gaa cgt	451																			
Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp Ala Gln Gln Glu Arg																				
105 110 115																				
gct tgg gtt att gat cgc cgc aac cag aac tac acc gca acc gac ggt	499																			
Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr Thr Ala Thr Asp Gly																				
120 125 130																				
ctt ggc gca tac gca gat agt tac cgc gag acc gca cag gtg ggc acc	547																			
Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr Ala Gln Val Gly Thr																				
135 140 145																				
acc atc cct gac gtt gtt cca gct gat gcc acc acc gtg aag tac aac	595																			
Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr Thr Val Lys Tyr Asn																				
150 155 160 165																				
gat ggc ggc aat gtg aat ggc aat tgg gca gag acc ggt gga gaa ctc	643																			
Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu Thr Gly Gly Glu Leu																				
170 175 180																				
gga tcc act gtt gat cta att gaa gct atc cgt cag cat gcc gca acc	691																			
Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg Gln His Ala Ala Thr																				
185 190 195																				
agc aac aat gcc aag gcg tac tac caa tac cca cgc ccc tac cgc tgg	739																			
Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro Arg Pro Tyr Arg Trp																				
200 205 210																				
act gaa tcc atc gaa cca gaa gcc tgg ggc gag ggc gtt gac atg cca	787																			
Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu Gly Val Asp Met Pro																				
215 220 225																				
gag tat gca aac cca ctg cgc aag gat gaa tcc gaa gct gcc agc gat	835																			
Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser Glu Ala Ala Ser Asp																				
230 235 240 245																				
ggc ggt ttc cct tcc gga cac acc tcc gca ggc ggc atg gca acc aac	883																			
Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly Gly Met Ala Thr Asn																				
250 255 260																				

ggc ctg gct tac gct ttc cca cag caa tac gat aaa ctg ctc atg act	931
Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp Lys Leu Leu Met Thr	
265 270 275	
gca gcg gaa atc ggc gaa agc cgc atc cag ctg ggc atg cac tct ccg	979
Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu Gly Met His Ser Pro	
280 285 290	
ctt gat gtt att ggc ggc cgt gtt cta tcc acc gcg att act gca ggt	1027
Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr Ala Ile Thr Ala Gly	
295 300 305	
gca ctt aat gat ccg aat ctc gac tcg gtg aag gct gaa gcc ttc gat	1075
Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys Ala Glu Ala Phe Asp	
310 315 320 325	
gat gct cag gca tgg atc agt aac cag agc gac atc acc acc aac act	1123
Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp Ile Thr Thr Asn Thr	
330 335 340	
cgc gat ttt gat gag caa ctc gcc gag tac acc aac ttc ctc acc ttc	1171
Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr Asn Phe Leu Thr Phe	
345 350 355	
ggc ttc gag cag tcc ggc gac acc acc caa gac atg cgc gtg cca aag	1219
Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp Met Arg Val Pro Lys	
360 365 370	
gga gct gag gct ctg ctg gaa acc cgc ctt ccg tac ctt gat gac gaa	1267
Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro Tyr Leu Asp Asp Glu	
375 380 385	
cag cgc cgt tgg gtt cta cat tcc act ggc ctc gag tcc ggt ttc cca	1315
Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu Glu Ser Gly Phe Pro	
390 395 400 405	
gta ctt gat gat gcc gaa ggt tgg ggc cgt ctc aac ctc tac gct gcc	1363
Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu Asn Leu Tyr Ala Ala	
410 415 420	
cag gct ggc tac agt gca ttc gat acc aac gtt gac gtc acc atg aat	1411
Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val Asp Val Thr Met Asn	
425 430 435	
gcc atc gac ggt ggc tac aac gcc aaa gac aac tgg caa aac gac atc	1459
Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn Trp Gln Asn Asp Ile	
440 445 450	
gag ggc gca gga tcc ctg acc aag aac ggt tcc ggt gaa ctc acc ctg	1507
Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser Gly Glu Leu Thr Leu	
455 460 465	
tca ggt gac aac tcc tac acc ggt gga acc acc atc acc gcg ggc acc	1555
Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr Ile Thr Ala Gly Thr	
470 475 480 485	
ttg gtt gct gca act gag tca gct ctg gga gca ggc gat ctc acc atc	1603
Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala Gly Asp Leu Thr Ile	
490 495 500	

aac gat ggt gca acc ttg aag atc acc cag cct gtc acc gtg gat gga. 1651  
 Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro Val Thr Val Asp Gly  
                   505                                  510                                  515

acc gca aac ctg gga gga act ctg cac gtt gcc ctt cct gtt ggc acc 1699  
 Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala Leu Pro Val Gly Thr  
                   520                                  525                                  530

aac cac gtc acc gtg atc gat gct gca tca att tcc ggt gaa ttt gat 1747  
 Asn His Val Thr Val Ile Asp Ala Ala Ser Ile Ser Gly Glu Phe Asp  
                   535                                  540                                  545

gag gtt att gtt gat ggc gca gtt gac gct cag gtg agc tac gac aac 1795  
 Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln Val Ser Tyr Asp Asn  
                   550                                  555                                  560                                  565

ggc tct gtc gtg att act aca ggc gca cct tct gat gac gta aag gaa 1843  
 Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser Asp Asp Val Lys Glu  
                                   570                                  575                                  580

act ggc tct tct gct ggc gga att ctt gcc atc gtg gca gcc ctg ggt 1891  
 Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile Val Ala Ala Leu Gly  
                                   585                                  590                                  595

ggc att gca gca ctg atc ttc ggt gca ttc acc cag ttt ggt ttc cca 1939  
 Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr Gln Phe Gly Phe Pro  
                   600                                  605                                  610

cca gca atc aag gaa atg ttc gac ctt taagccttcg ccaacccac 1986  
 Pro Ala Ile Lys Glu Met Phe Asp Leu  
                   615                                  620

ggc 1989

<210> 416  
 <211> 622  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 416  
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Ala Ser Thr Ile Ile Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala  
                   20                                  25                                  30

Leu Leu Asp Ala Ser Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr  
                   35                                  40                                  45

Tyr Val Asp Ala Trp Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser  
                   50                                  55                                  60

Ser Asn Ala Ala Val Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr  
                   65                                  70                                  75                                  80

Pro Gly Glu Glu Trp Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu  
                   85                                  90                                  95

Asp Ser Asn Ile Ala Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp  
                   100                                  105                                  110

Ala Gln Gln Glu Arg Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr  
115 120 125

Thr Ala Thr Asp Gly Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr  
130 135 140

Ala Gln Val Gly Thr Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr  
145 150 155 160

Thr Val Lys Tyr Asn Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu  
165 170 175

Thr Gly Gly Glu Leu Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg  
180 185 190

Gln His Ala Ala Thr Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro  
195 200 205

Arg Pro Tyr Arg Trp Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu  
210 215 220

Gly Val Asp Met Pro Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser  
225 230 235 240

Glu Ala Ala Ser Asp Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly  
245 250 255

Gly Met Ala Thr Asn Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp  
260 265 270

Lys Leu Leu Met Thr Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu  
275 280 285

Gly Met His Ser Pro Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr  
290 295 300

Ala Ile Thr Ala Gly Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys  
305 310 315 320

Ala Glu Ala Phe Asp Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp  
325 330 335

Ile Thr Thr Asn Thr Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr  
340 345 350

Asn Phe Leu Thr Phe Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp  
355 360 365

Met Arg Val Pro Lys Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro  
370 375 380

Tyr Leu Asp Asp Glu Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu  
385 390 395 400

Glu Ser Gly Phe Pro Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu  
405 410 415

Asn Leu Tyr Ala Ala Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val  
420 425 430



Asp Val Thr Met Asn Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn  
 435 440 445  
 Trp Gln Asn Asp Ile Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser  
 450 455 460  
 Gly Glu Leu Thr Leu Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr  
 465 470 475 480  
 Ile Thr Ala Gly Thr Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala  
 485 490 495  
 Gly Asp Leu Thr Ile Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro  
 500 505 510  
 Val Thr Val Asp Gly Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala  
 515 520 525  
 Leu Pro Val Gly Thr Asn His Val Thr Val Ile Asp Ala Ala Ser Ile  
 530 535 540  
 Ser Gly Glu Phe Asp Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln  
 545 550 555 560  
 Val Ser Tyr Asp Asn Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser  
 565 570 575  
 Asp Asp Val Lys Glu Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile  
 580 585 590  
 Val Ala Ala Leu Gly Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr  
 595 600 605  
 Gln Phe Gly Phe Pro Pro Ala Ile Lys Glu Met Phe Asp Leu  
 610 615 620

<210> 417  
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<220>  
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 <222> (101)..(397)  
 <223> RXA01453

<400> 417  
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 Met Ala Gln Lys Leu  
 1 5  
 tac ccg ccg att cac cct ggt gag att ctc atg gag gac ttc atc aag 163  
 Tyr Pro Pro Ile His Pro Gly Glu Ile Leu Met Glu Asp Phe Ile Lys  
 10 15 20  
 ggc ttc ggc ctc aca cag aac aag gtc gcc gta tcg atc ggg gtg cct 211  
 Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val Ser Ile Gly Val Pro  
 25 30 35

ccg cga cgc atc aac gag atc gtg cac ggc aag cga tcc atc acg gcc 259  
Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ser Ile Thr Ala  
40 45 50

gat acg gct ctg cgt ctc ggg cgg tac ttc ggt atc gac ccg cag ttc 307  
Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly Ile Asp Pro Gln Phe  
55 60 65

tgg ctg agc ctt cag act cag tac gag ttg gag ctc gat cgc gac gcc 355  
Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu Leu Asp Arg Asp Ala  
70 75 80 85

ggt gca gcg act tac gca cag atc acg ccg ctg aag gtc gcg 397  
Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu Lys Val Ala  
90 95

tgagctcggg gccagaaaa cat 420

<210> 418  
<211> 99  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 418  
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Ser Ile Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys  
35 40 45

Arg Ser Ile Thr Ala Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly  
50 55 60

Ile Asp Pro Gln Phe Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu  
65 70 75 80

Leu Asp Arg Asp Ala Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu  
85 90 95

Lys Val Ala

<210> 419  
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<212> DNA  
<213> Corynebacterium glutamicum

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<222> (101)..(922)  
<223> RXA01824

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acggccgacc actcatcgtg cccacagaca ggagaaactc	atg aaa gaa acc gac	115
	Met Lys Glu Thr Asp	
	1 5	
aac cta ctg cgc gaa aac tcc cac gac cgc gac atc tct gaa atc gtc	163	
Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp Ile Ser Glu Ile Val		
10 15 20		
gcc acc atc act gcc ctt gac cac cca tca ccc tca ctt ctg cga ttc	211	
Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro Ser Leu Leu Arg Phe		
25 30 35		
aca gct ttt gtt cca gga tca gca aac aac cca gtg tgg gca gaa gcc	259	
Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro Val Trp Ala Glu Ala		
40 45 50		
aac gtg gca atc agg ctt tac ctc agc gaa gaa ttc gac gac gcc acc	307	
Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu Phe Asp Asp Ala Thr		
55 60 65		
cgc gtc tac acc gtc cga tcc ttt gat gcc gca act gaa agc atc gtg	355	
Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala Thr Glu Ser Ile Val		
70 75 80 85		
gtg gat gtg gtt caa cac cac cac gaa agc ccc atg atg cgc tgg tca	403	
Val Asp Val Val Gln His His His Glu Ser Pro Met Met Arg Trp Ser		
90 95 100		
gac acc gta aaa atc aac gac acc ctc gtg ctc acc gga ccc cgc cca	451	
Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu Thr Gly Pro Arg Pro		
105 110 115		
cac ttt gtc atc ccc gaa ggc gaa caa gca gca ctc ttc ctt gat gac	499	
His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala Leu Phe Leu Asp Asp		
120 125 130		
acc gcc atc ccc gct ctc gcc gct att ttg gat caa tgg cca aca gat	547	
Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp Gln Trp Pro Thr Asp		
135 140 145		
ctt cgt ggc aaa gga tgg gtt gtc act gac gat ccc gca gcc ttc gat	595	
Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp Pro Ala Ala Phe Asp		
150 155 160 165		
gaa cta ccc agc atc gac gga ctg gaa ctg aac ctg ctc gcg ccg gga	643	
Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn Leu Leu Ala Pro Gly		
170 175 180		
tca gat cca act gtt cag cca ctt gcc caa cag gca tat gac ctg gaa	691	
Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln Ala Tyr Asp Leu Glu		
185 190 195		
aac cca gaa act tac gtg gtg tgg gca gcc ggc gag cga gat gaa ata	739	
Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly Glu Arg Asp Glu Ile		
200 205 210		
aaa tcc atc cgc agg cac ttc cgc aag cag gtg gga ttg gaa aaa gat	787	
Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val Gly Leu Glu Lys Asp		
215 220 225		
gca gtg gcc gtg ttt ggg tac tgg aaa tac aac acc acc aac act cag	835	

Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn Thr Thr Asn Thr Gln  
 230 235 240 245

atc gat gca gtc cgc aaa gaa aac tac atg aag atg ctc tct gaa ggg 883  
 Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys Met Leu Ser Glu Gly  
 250 255 260

cta cag ctg gaa aac ttc gac gac ctc tca ttg gag att taaggggtcg 932  
 Leu Gln Leu Glu Asn Phe Asp Asp Leu Ser Leu Glu Ile  
 265 270

agtttttaga atg 945

&lt;210&gt; 420

&lt;211&gt; 274

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 420

Met Lys Glu Thr Asp Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp  
 1 5 10 15

Ile Ser Glu Ile Val Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro  
 20 25 30

Ser Leu Leu Arg Phe Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro  
 35 40 45

Val Trp Ala Glu Ala Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu  
 50 55 60

Phe Asp Asp Ala Thr Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala  
 65 70 75 80

Thr Glu Ser Ile Val Val Asp Val Val Gln His His His Glu Ser Pro  
 85 90 95

Met Met Arg Trp Ser Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu  
 100 105 110

Thr Gly Pro Arg Pro His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala  
 115 120 125

Leu Phe Leu Asp Asp Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp  
 130 135 140

Gln Trp Pro Thr Asp Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp  
 145 150 155 160

Pro Ala Ala Phe Asp Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn  
 165 170 175

Leu Leu Ala Pro Gly Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln  
 180 185 190

Ala Tyr Asp Leu Glu Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly  
 195 200 205

Glu Arg Asp Glu Ile Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val  
 210 215 220

Gly Leu Glu Lys Asp Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn  
225 230 235 240

Thr Thr Asn Thr Gln Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys  
245 250 255

Met Leu Ser Glu Gly Leu Gln Leu Glu Asn Phe Asp Asp Leu Ser Leu  
260 265 270

Glu Ile

<210> 421

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXA01832

<400> 421

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tggaacaccc aacttattga gaaaaggagg tcgcaaagtt atg gct act tcg aat 115  
Met Ala Thr Ser Asn  
1 5

cgg ata gct aat gct atg aac agt ttg gcc aag ctg gac agt tct atg 163  
Arg Ile Ala Asn Ala Met Asn Ser Leu Ala Lys Leu Asp Ser Ser Met  
10 15 20

caa cgc ggc ctt gat aat gcg ttg gcg ttt gtt ttc cgt ggt cgc gtt 211  
Gln Arg Gly Leu Asp Asn Ala Leu Ala Phe Val Phe Arg Gly Arg Val  
25 30 35

gtt ccg gct gag ctt gag gag ctt ttg aag caa gag gct gag gac aat 259  
Val Pro Ala Glu Leu Glu Glu Leu Lys Gln Glu Ala Glu Asp Asn  
40 45 50

gtg gtt cat act gag ttt ggc tat gtt gag gcg ccg aat gtt ttt aag 307  
Val Val His Thr Glu Phe Gly Tyr Val Glu Ala Pro Asn Val Phe Lys  
55 60 65

gtt tcg gtg agc ccg aac gat ttt agt aat ctt gtc gat cgt ttt cct 355  
Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu Val Asp Arg Phe Pro  
70 75 80 85

gat cag ccg gct cgt ttt ggt gat cag atg atg agg ttc tgc agg aac 403  
Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met Arg Phe Cys Arg Asn  
90 95 100

agt ggc tgg acg ttg gtt ggg ccg gtg att gtg ttg att gaa gag gat 451  
Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val Leu Ile Glu Glu Asp  
105 110 115

tct tcg ttg cac acg ggc cag ttg aag tcg gtt tcg gag aag gat ccg 499  
Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val Ser Glu Lys Asp Pro

120	125	130	
gat ccg gag tta agt agc ggt tat ctg cct ttg gaa ggc gac ggc atc Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu Glu Gly Asp Gly Ile 135 140 145			547
ctg cct gtc gca gaa agt gag tct aag aac gtg tct gac agt tcc cct Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val Ser Asp Ser Ser Pro 150 155 160 165			595
tac act ggt acg gag ttt ttg ccg gcg caa tca gcg gat cgc cct ttg Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser Ala Asp Arg Pro Leu 170 175 180			643
gtt cag ggt gtg ccg cag tct cag gtt gat gcg aat cgc cag gct gcg Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala Asn Arg Gln Ala Ala 185 190 195			691
atg aag ccc gcg ggc cct acg gtg act ttg ctg ctg cag gat ggt tcg Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu Leu Gln Asp Gly Ser 200 205 210			739
agc cgg act tat ttg gtt ccg gag ggt tcg aac atc att ggt cgt agt Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn Ile Ile Gly Arg Ser 215 220 225			787
aat gat gcg gat ctt cgt ttg ccg gat act ggt gtg tct cgt cag cat Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly Val Ser Arg Gln His 230 235 240 245			835
gtg gag atc acg tgg gat ggc ccg gat gcc att ttg gtt gat ttg aag Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile Leu Val Asp Leu Lys 250 255 260			883
tcg act aat ggc acc acg gtg aat gac act cct gtg gat aat tgg ttg Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro Val Asp Asn Trp Leu 265 270 275			931
ttg gct gat ggt gat gtc att acg gtg ggt cat tcc aat atc gaa gtt Leu Ala Asp Gly Asp Val Ile Thr Val Gly His Ser Asn Ile Glu Val 280 285 290			979
cggt att gtt agt ccc tagagggaga ggttgatcaa tgg Arg Ile Val Ser Pro 295			1017

&lt;210&gt; 422

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 422

Met	Ala	Thr	Ser	Asn	Arg	Ile	Ala	Asn	Ala	Met	Asn	Ser	Leu	Ala	Lys
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Leu	Asp	Ser	Ser	Met	Gln	Arg	Gly	Leu	Asp	Asn	Ala	Leu	Ala	Phe	Val
	20							25					30		

Phe	Arg	Gly	Arg	Val	Val	Pro	Ala	Glu	Leu	Glu	Glu	Leu	Leu	Lys	Gln
	35						40					45			

Glu Ala Glu Asp Asn Val Val His Thr Glu Phe Gly Tyr Val Glu Ala  
50 55 60

Pro Asn Val Phe Lys Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu  
65 70 75 80

Val Asp Arg Phe Pro Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met  
85 90 95

Arg Phe Cys Arg Asn Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val  
100 105 110

Leu Ile Glu Glu Asp Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val  
115 120 125

Ser Glu Lys Asp Pro Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu  
130 135 140

Glu Gly Asp Gly Ile Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val  
145 150 155 160

Ser Asp Ser Ser Pro Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser  
165 170 175

Ala Asp Arg Pro Leu Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala  
180 185 190

Asn Arg Gln Ala Ala Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu  
195 200 205

Leu Gln Asp Gly Ser Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn  
210 215 220

Ile Ile Gly Arg Ser Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly  
225 230 235 240

Val Ser Arg Gln His Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile  
245 250 255

Leu Val Asp Leu Lys Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro  
260 265 270

Val Asp Asn Trp Leu Leu Ala Asp Gly Asp Val Ile Thr Val Gly His  
275 280 285

Ser Asn Ile Glu Val Arg Ile Val Ser Pro  
290 295

&lt;210&gt; 423

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(667)

&lt;223&gt; RXA02533

&lt;400&gt; 423

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<210> 424
<211> 189
<212> PRT
<213> Corynebacterium glutamicum
<400> 424
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<400> 424



Met Glu Asp Asp Leu Ser Ala Ala Leu Val Lys Ala Leu Phe Asp Ala  
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 20 25 30  
 Val Ser Arg Ala Met Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro  
 35 40 45  
 Ser Ala Ala Leu Leu Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu  
 50 55 60  
 Ser Glu Leu Ile Ala Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg  
 65 70 75 80  
 Arg Ser Lys Gln Ser Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg  
 85 90 95  
 Arg Ala Val Ser Gln Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val  
 100 105 110  
 Met Leu Pro Pro Gly Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg  
 115 120 125  
 Phe Met Asp Gln Val Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr  
 130 135 140  
 Glu Gly Glu Glu Val His Glu Leu Ser Thr Gly Asp Cys Leu Arg Phe  
 145 150 155 160  
 Gly Pro Pro Arg Asp Thr Asp Phe Ala Asn Pro Thr Thr Val Ala Thr  
 165 170 175  
 Arg Tyr Leu Val Ala Leu Asp Lys Arg Val Pro Arg Ala  
 180 185

&lt;210&gt; 425

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1012)

&lt;223&gt; RXN02727

&lt;400&gt; 425

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ctaaagcagc aggtcgaaga gctagaggcg caggttgccg gtg gtc ctt ctt ccg 115  
 Val Val Leu Leu Pro 5  
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ctg cta gtt cct caa ctg cag gtg cag cca cag ttg cag ctt cca agt 163  
 Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln Leu Gln Leu Pro Ser 20  
 10 15

ctg ttg acg agg cag cgc tgc gca agg aaa tca aag aga agc tgc gct 211  
 Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser Lys Arg Ser Cys Ala 35  
 25 30

ccg aat acg gca tcc aag ctc gat gat gcc tcc aag gcc gct cag aag	259
Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser Lys Ala Ala Gln Lys	
40 45 50	
gct caa aac gat gcg aag tcc gct caa gat cag cta cag cgt gca caa	307
Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln Leu Gln Arg Ala Gln	
55 60 65	
gct gac gca aag gca gct cgc gac gaa gct gaa aag gcc aag gct gaa	355
Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu Lys Ala Lys Ala Glu	
70 75 80 85	
gct aag tca gca gca tcc tcc agc acc act aag gca gca gcg gtt ggc	403
Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys Ala Ala Ala Val Gly	
90 95 100	
gct gtc ggc gct ggc acc gga gca gca gtt gct aca ggt gct gca aat	451
Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala Thr Gly Ala Ala Asn	
105 110 115	
gtg gac acc cac atg cag gca gcg aag gtt ctg gga ctc gca cag gaa	499
Val Asp Thr His Met Gln Ala Ala Lys Val Leu Gly Leu Ala Gln Glu	
120 125 130	
atg gca gac cgc ctg acc tca gag gct cgc tcc gaa tcc aag tcc atg	547
Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser Glu Ser Lys Ser Met	
135 140 145	
ctg gac gag gct cgc gaa gca gca gag aag cag atc gag gaa gca aac	595
Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln Ile Glu Glu Ala Asn	
150 155 160 165	
agc acc tcc aac cgc act ctg gaa gat gct cgc gca aac gct gag aag	643
Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg Ala Asn Ala Glu Lys	
170 175 180	
cag atc gct gaa gcg cag aac cgc gct gac act ctg gtc aac gaa gct	691
Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr Leu Val Asn Glu Ala	
185 190 195	
gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca	739
Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala	
200 205 210	
gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa	787
Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln	
215 220 225	
gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac	835
Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His	
230 235 240 245	
acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc	883
Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln Asn Ala Leu Glu Thr	
250 255 260	
cgc atc gcg gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg	931
Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu	
265 270 275	

aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc 979  
Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser  
280 285 290

tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032  
Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu  
295 300

ctt 1035

<210> 426

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Val Val Leu Leu Pro Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln  
1 5 10 15

Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser  
20 25 30

Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser  
35 40 45

Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln  
50 55 60

Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu  
65 70 75 80

Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys  
85 90 95

Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala  
100 105 110

Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu  
115 120 125

Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser  
130 135 140

Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln  
145 150 155 160

Ile Glu Glu Ala Asn Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg  
165 170 175

Ala Asn Ala Glu Lys Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr  
180 185 190

Leu Val Asn Glu Ala Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala  
195 200 205

Glu Lys Lys Ser Ala Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu  
210 215 220

Ala Gln Ile Arg Gln Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp  
225 230 235 240



gga agc ttc gcc gag caa aat agg gcc ggc gtg aag gcg tcg gcg atc 499  
 Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val Lys Ala Ser Ala Ile  
 120 125 130

tcg cgc cgc gcc gaa caa tcc gcg ctc tac aag gcg aaa aaa atc ggc 547  
 Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys Ala Lys Lys Ile Gly  
 135 140 145

gaa ttc gcc gag cgc gcc cca cgc gtc aaa gag cgg caa gag gca cat 595  
 Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu Arg Gln Glu Ala His  
 150 155 160 165

tgg tgg cca cgg ttg tca cgc acg caa ggc acc gca ggc gtt tta cgc 643  
 Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr Ala Gly Val Leu Arg  
 170 175 180

tta gcg acg gac gcc tct acc gat ggg gtc ttc cgc ggc gcc atg tgc 691  
 Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe Arg Gly Ala Met Cys  
 185 190 195

ttc gta gcc tca aac ggc gac tac ctc ctg gag acc caa gac acc acc 739  
 Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu Thr Gln Asp Thr Thr  
 200 205 210

gca agc tcc gac gaa tta gaa ctc gaa agc atc acc cac gcc ctg atc 787  
 Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile Thr His Ala Leu Ile  
 215 220 225

tac ctc aaa acc atc ggc gcg acc caa gcc atc atc gaa tcc gac agc 835  
 Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile Ile Glu Ser Asp Ser  
 230 235 240 245

aaa gcc gca ctt gaa gcc atc gac ttc atc ctc aac aac cga ccg cgc 883  
 Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu Asn Asn Arg Pro Arg  
 250 255 260

cgg ggc agg tgg cgc ggc atc acc gca tgc gcc cgc aac cgg ttc cgg 931  
 Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala Arg Asn Arg Phe Arg  
 265 270 275

gat gcc tgg gaa gcg ctt atc gac gac tgc gtt gtg gaa tta tcc cgc 979  
 Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val Val Glu Leu Ser Arg  
 280 285 290

gta cta ggg cac gcc ggg gat cca ctg aac caa gca gcc gac caa atc 1027  
 Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln Ala Ala Asp Gln Ile  
 295 300 305

gca tac atg ggc atg cgc gcc gta att ttt gaa caa aaa tcc gca cac 1075  
 Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu Gln Lys Ser Ala His  
 310 315 320 325

ccc aca ttg ctc aaa gga att gac aag gcg ctt cgc aag gcc gag 1120  
 Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu Arg Lys Ala Glu  
 330 335 340

taaggtgggc aacgagtcgg tga 1143

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 428

Met Lys Ser Ile Asp Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr  
1 5 10 15  
Tyr Gln Ser Arg Lys Ile Thr Asp Glu Met Val Ala Arg Pro Val His  
20 25 30  
Val Ala Ile Ala Leu Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly  
35 40 45  
Lys Ile Glu Gly Trp Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe  
50 55 60  
Val Arg Ser Gly Gln Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val  
65 70 75 80  
Ser Met Leu Lys Ser Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile  
85 90 95  
Val Thr Gly Arg Arg Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu  
100 105 110  
Asn Tyr Leu Val Thr Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val  
115 120 125  
Lys Ala Ser Ala Ile Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys  
130 135 140  
Ala Lys Lys Ile Gly Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu  
145 150 155 160  
Arg Gln Glu Ala His Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr  
165 170 175  
Ala Gly Val Leu Arg Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe  
180 185 190  
Arg Gly Ala Met Cys Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu  
195 200 205  
Thr Gln Asp Thr Thr Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile  
210 215 220  
Thr His Ala Leu Ile Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile  
225 230 235 240  
Ile Glu Ser Asp Ser Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu  
245 250 255  
Asn Asn Arg Pro Arg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala  
260 265 270  
Arg Asn Arg Phe Arg Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val  
275 280 285  
Val Glu Leu Ser Arg Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln  
290 295 300

Ala Ala Asp Gln Ile Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu  
305 310 315 320

Gln Lys Ser Ala His Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu  
325 330 335

Arg Lys Ala Glu  
340

<210> 429

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXN01966

<400> 429

gctgtccaag gccatgaatt ttgtgtcctc tggtgtcca accgctgtgc tctcccctgt 60  
tatgggctgg gtttataaga agatgggtta gtttttaaaa gtg tct gaa tct gaa 115  
Val Ser Glu Ser Glu  
1 5  
aac aac aca aca cca gca gtc gca gct cgc gat gac cgt ctg gtc tgg 163  
Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp Asp Arg Leu Val Trp  
10 15 20  
gtc gat ctg gaa atg act ggt cta gat ttg aag cgc cac gtg atc gtg 211  
Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys Arg His Val Ile Val  
25 30 35  
gag gtt gcg gcg ttg gtc act gac gct aac ctc aac gtt ttg ggc gag 259  
Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu Asn Val Leu Gly Glu  
40 45 50  
ggc gtg gac ttg gtt gtt cac gca act gaa gaa gag ctc gcg cag atg 307  
Gly Val Asp Leu Val Val His Ala Thr Glu Glu Glu Leu Ala Gln Met  
55 60 65  
gat gat ttt gtc acc aac atg cac gaa tcc tct ggg ctg act gag cag 355  
Asp Asp Phe Val Thr Asn Met His Glu Ser Ser Gly Leu Thr Glu Gln  
70 75 80 85  
atc cgg gaa tcc gcg gtc acg ttg aag gaa gcc gaa gat gct gtg ctc 403  
Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala Glu Asp Ala Val Leu  
90 95 100  
gca ttg att gaa aag cac tgc gat cca gcc cat cct gca ccg cta gct 451  
Ala Leu Ile Glu Lys His Cys Asp Pro Ala His Pro Ala Pro Leu Ala  
105 110 115  
ggg aac tcc att gcc act gac cgc gcg ttt atc cgc gaa cat atg cca 499  
Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile Arg Glu His Met Pro  
120 125 130  
cgt ctt gat gag gcc ctg cat tac cgc atg gtg gat gtg tcc tcg gtg 547

Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val Asp Val Ser Ser Val  
 135 140 145  
 aag gaa ttg gcg cgt cgc tgg tac cca cgc gtg tac tac aag cag ccg 595  
 Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val Tyr Tyr Lys Gln Pro  
 150 155 160 165  
 gag aag ggt ttg gcg cac cgc gcg ttg gcg gac att gtg gag tcg att 643  
 Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp Ile Val Glu Ser Ile  
 170 175 180  
 cgg gag ttg gat tac tac cgt cgc tca ttt ttt gtt gca gag cct ggt 691  
 Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe Val Ala Glu Pro Gly  
 185 190 195  
 cct acc tct gag cag tgc gca gat gat gcg cag gca gcg gtg gac cgt 739  
 Pro Thr Ser Glu Gln Cys Ala Asp Ala Gln Ala Val Asp Arg  
 200 205 210  
 ttt gca ccc tac ttt gat tagagggttt taagcagcct ggt 780  
 Phe Ala Pro Tyr Phe Asp  
 215

&lt;210&gt; 430

&lt;211&gt; 219

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 430

Val Ser Glu Ser Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp  
 1 5 10 15  
 Asp Arg Leu Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys  
 20 25 30  
 Arg His Val Ile Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu  
 35 40 45  
 Asn Val Leu Gly Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu  
 50 55 60  
 Glu Leu Ala Gln Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser  
 65 70 75 80  
 Gly Leu Thr Glu Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala  
 85 90 95  
 Glu Asp Ala Val Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His  
 100 105 110  
 Pro Ala Pro Leu Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile  
 115 120 125  
 Arg Glu His Met Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val  
 130 135 140  
 Asp Val Ser Ser Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val  
 145 150 155 160  
 Tyr Tyr Lys Gln Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp



61

	165	170	175
Ile Val Glu Ser Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe			
	180	185	190
Val Ala Glu Pro Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln			
	195	200	205
Ala Ala Val Asp Arg Phe Ala Pro Tyr Phe Asp			
	210	215	

&lt;210&gt; 431

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 431

ggaaacagta tgaccatg

18

&lt;210&gt; 432

&lt;211&gt; 17

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 432

gtaaaacgac ggccagt

17